

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2002, 18:25:39 : Search time 1945 Seconds  
(without alignments)  
4725.669 Million cell updates/sec

Title: US-09-896-301-1

Perfect score: 681  
Sequence: 1 gactacgctgctgcgcagag.....cctatgaagccccaattc 681

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 674847542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estdb:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_hic:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429.4	53.1	798	10	BG581975 EST483712
2	404.8	59.4	767	10	B1933999 EST552888
3	396.8	58.3	646	9	AM774064 EST31653
4	393.4	57.8	815	9	BE131139 L48-1090T
5	384	56.4	868	9	BG44553 GA_EB003
6	382	56.1	966	9	BE055631 GA_EA003
7	368.8	54.2	775	9	BE034856 MLO5C12 M
8	367.8	54.0	741	10	B1309709 EST531119
9	365.6	53.7	706	10	BF479593 L48-3281T
10	359.4	52.8	668	9	AM776306 EST335371
11	358.6	52.7	654	10	BE584282 7-3E-HA P
12	357	52.4	752	10	B131879 EST531362
13	356	52.3	710	10	B1931078 EST550967
14	353.8	52.0	695	9	AM584547 N210609e
15	353.8	52.0	702	9	BE130849 L48-1796T
16	353.6	51.9	816	10	BG645633 EST507252
17	351.4	51.6	718	10	B1308364 EST529774

18	351.4	51.6	733	9	BE130942 L48-1870T
19	347	51.0	925	10	BG444019 GA_EA002
20	346.8	50.9	966	10	BF479791 L48-3533T
21	342.8	50.3	597	9	A1729996 BNGH1592
22	342.8	50.3	692	10	BM299764 MCR052G06
23	342.2	50.2	630	9	A1727312 BNGH1774
24	341.2	50.1	632	10	B1308198 EST529608
25	340.8	50.0	595	9	A1730550 BNGH1706
26	339.8	49.9	693	10	BG440009 GA_EA000
27	339.6	49.9	1013	10	BG446150 GA_EA003
28	339	49.8	714	10	BG440720 GA_EA000
29	338.8	49.8	825	10	BF621546 HVSME001
30	338.4	49.7	792	10	B1179439 EST5520384
31	338	49.6	566	10	BE608803 9096407 Y
32	337.2	49.5	745	9	AM299054 EST305728
33	337	49.5	857	10	BG441892 GA_EA001
34	336.6	49.4	629	10	BF566797 su62907 Y
35	336.2	49.4	673	10	B1932259 EST552148
36	336.2	49.4	746	10	B1933094 EST552983
37	335.8	49.3	516	10	B1315838 9a63h11
38	334.2	49.1	653	10	BM437064 VVA013F08
39	333.8	49.0	697	10	BG441784 GA_EA001
40	331.8	48.7	699	10	BM299670 MCR053F03
41	330	48.5	735	10	BF268285 GA_EB000
42	326.6	48.0	691	10	BG440379 GA_EA000
43	326.6	48.0	697	10	BG440350 GA_EA000
44	325.8	47.8	658	10	BF270330 GA_EB002
45	325.6	47.8	681	10	BG443534 GA_EA002

#### ALIGNMENTS

RESULT 1  
BG581975 798 bp mRNA linear EST 11-APR-2001  
EST483712 GVN Medicago truncatula cDNA clone gVN-66124 5' end,  
LOCUS BG581975  
DEFINITION BG581975.1 GI:13597039  
ACCESSION BG581975  
VERSION BG581975.1  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.

REFERENCE 1 (bases 1 to 798)  
AUTHORS Fedorova,M., Pierzon,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town  
C.D., Van Aken,S., Uterback,T., Cho,J. and Fraser,C.M.  
TITLE ESTs from one month old nitrogen-fixing root nodules of Medicago  
truncatula, 2001  
JOURNAL Unpublished (2001)  
COMMENT Contact: Carroll P. Vance  
Department of Agronomy and Plant Genetics  
University of Minnesota  
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA  
Tel: 612 625 5715  
Fax: 651-649-5058  
Email: Vance004@maroon.tc.umn.edu  
University of Minnesota name: M83038e TIGR sequence name:  
MCDP007K More information is available at: <http://www.medicago.org>  
Seq primer: Sknnd (CTA gNA gNA gNA gAT CC).

#### FEATURES

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/organism="Medicago truncatula"  
/cultivar="genotype A17"  
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/clone="pgVN-66124"  
/clone\_lib="GVN"  
/tissue\_type="N2-fixing root nodules"  
/dev\_stage="effective root nodules harvested one month  
post inoculation with Sinorhizobium meliloti"



Db 509 CAATCAGTTTCAATTAAGGCTTAATCTAGTATGCAAGCAATCTCAAGATATTGGGCG 568  
 Qy 541 CAAATCGCAAGCAAGCAACTATCTGCATGGCCAGGCTTCCCTTCAAGCACTCTT 600  
 Db 569 CAAATTTGGCAAGCAATCTTATATGATGGTCAAGCTTTCATTTATGTCACACACA 628  
 Qy 601 AGTATGTCGACATCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTTGGCAA 660  
 Db 629 AGTATGTCGACATCTCACTGCTTAATCTGCTTCCCAATTTGGCAATTTGGCAA 688  
 Qy 661 ACCTATGAGGCCCTCAATT 680  
 Db 689 ACTTTGGAAGGGGCTCAATT 708  
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 LOCUS AWS74064  
 DEFINITION EST13655 GVN Medicago truncatula cdna clone pgvn-51c8, mRNA  
 sequence.  
 ACCESSION AWS74064 GI:7238797  
 VERSION AWS74064.1 GI:7238797  
 KEYWORDS EST.  
 SOURCE Medicago truncatula  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 646)  
 REFERENCE  
 AUTHORS Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Peng  
 H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S.,  
 Holt, I.E. and Fraser, C.M.  
 TITLES ESTs from one month old nitrogen-fixing root nodules of Medicago  
 truncatula  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Carroll P. Vance  
 Department of Agronomy and Plant Genetics  
 University of Minnesota  
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA  
 Tel: 612 625 5715  
 Fax: 651-649-5058  
 Email: Vance004@maroon.tc.umn.edu  
 Minnesota EST name: M252962e  
 TIGR sequence name: MTCAR16TK  
 More information is available at: <http://chryslr.tamu.edu/medicago/>  
 Seq primer: SKmod (CTA gaa CTA gta gat CC).  
 Location/Qualifiers  
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 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone="pgvn-51c8"  
 /clone\_lib="GVN"  
 /tissue\_type="N2-fixing root nodules"  
 /dev\_stage="effective root nodules harvested one month  
 post inoculation with Sinorhizobium meliloti"  
 /lab\_host="E. coli strain XL0R"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 effective root nodules harvested one month post  
 inoculation with Sinorhizobium meliloti. The cDNA was  
 directionally ligated into the uni-ZAP XR vector from  
 streptagene and packaged using GigaPack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-ZAP phage using Ex-Assist  
 helper phage and propagated in XL0R cells."  
 BASE COUNT 186 a 134 c 144 g 181 t 1 others  
 Query Match 58.3%; Score 396.8; DB 9; Length 646;

Best Local Similarity 77.6%; Pred. No. 6e-110;  
 Matches 479; Conservative 0; Mismatches 138; Indels 0; Caps 0;  
 Qy 64 ATGGGTGAGCTTGGGGTATGGGAATTTATACGCCAAGGGATGACGACACAGCTG 123  
 Db 2 ATGGGAGGGGCTTGGTATGGAATTTATATACCAAGGCTATGGAACCACTGCT 61  
 Qy 124 GCGGTGACGACGCTGCTTTTAAACAATGATTAAGTTGGTGGCTTGGTGAATGACT 183  
 Db 62 GCAGTAAGCAGCTGCTTTTCAACAATGATTAAGTTGGTGGCTTGGTGAATGACT 121  
 Qy 184 TGTACAAAGACCTTAATGATGCTTCCGGGAACCTATAGGCTACCTGACCAACTTT 243  
 Db 122 TGTACAGAGGACCTTAATGATGCTTCCGGGAACCTATAGGCTACCTGACCAACTTT 181  
 Qy 244 TGGCCTCTACTTGTGCTCTCTTAAACAATGATTAAGTTGGTGGCTTGGTGAATGACT 303  
 Db 182 TGGCCTCTACTTGTGCTCTCTTAAACAATGATTAAGTTGGTGGCTTGGTGAATGACT 241  
 Qy 304 CACTTCGACATGCTGACGCTGCTTCCCTTCAATCGCTCAATACGAGCTGATGCTG 363  
 Db 242 CACTTCGATCTTGTGACGCTGCTTCCCTTCAATCGCTCAATACGAGCTGATGCTG 301  
 Qy 364 CCGCTCTCTTGTGATGAGGTATGAGGAAGGAGTGAAGGCTTCAATCAATCAAT 423  
 Db 302 CCTATTCTCTTGAAGAAGAGTACCTGTTTGAAGAAGGAGTGAAGGCTTCAATCAATCAAT 361  
 Qy 424 GGCACATCACTTCAATCAATGCTTGTGATCAACAAGCTGCTGCGCAGGAGCTCCAC 483  
 Db 362 GGCACATCACTTCAATCAATGCTTGTGATCAACAAGCTGCTGCGCAGGAGCTCCAC 421  
 Qy 484 TCTGTGATGATGAAGGGGCTGACGCTGATGAGGCAATGCTCAATGATGAGGAGGAG 543  
 Db 422 TCTGTGATGATGAAGGGGCTGACGCTGATGAGGCAATGCTCAATGATGAGGAGGAG 481  
 Qy 544 AACTGCAAGCAAGCAATCAATGATGAGGCAAGGCTTCTTCAATGATGAGGAGGAG 603  
 Db 482 AACTGCAAGCAAGCAATCAATGATGAGGCAAGGCTTCTTCAATGATGAGGAGGAG 541  
 Qy 604 GATGCTGACATCTGACGCTGATATATGCTTCTTCAATGATGAGGAGGAGGAG 663  
 Db 542 GATGCTGACATCTGACGCTGATATATGCTTCTTCAATGATGAGGAGGAGGAG 601  
 Qy 664 TATGAAGGCCCTCAATT 680  
 Db 602 TTTACAGGGGGCTCAATT 618  
 RESULT 4  
 BE131139 815 bp mRNA linear EST 20-FEB-2001  
 LOCUS BE131139  
 DEFINITION L48-109073 Ice plant Lambda Uni-Zap XR expression library, 48 hours  
 NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1090  
 5', mRNA sequence.  
 ACCESSION BE131139  
 VERSION BE131139.1 GI:8578502  
 KEYWORDS EST.  
 SOURCE Common ice plant.  
 ORGANISM Mesembryanthemum crystallinum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllidae; Caryophyllales; Alzaceae; Mesembryanthemum.  
 1 (bases 1 to 815)  
 REFERENCE  
 AUTHORS Cushman, J.C.  
 TITLES An expressed sequence tag database for the common ice plant.  
 JOURNAL Mesembryanthemum crystallinum  
 COMMENT Unpublished (1997)  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650

Email: jecushman@unr.edu

PCR Primers

FORWARD: T7

BACKWARD: T3

Plate: L48-11 row: H column: 6

Seq primer: T3

High quality sequence stop: 350

POLY-A-NO.

FEATURES location/Qualifiers

SOURCE

1. 815

/organism="Mesembryanthemum crystallinum"

/db\_xref="taxon:3544"

/clone="L48-1090"

/clone\_lib="Ice plant Lambda Uni-Zap XR expression library

, 48 hours NaCl treatment"

/tissue\_type="Leaf, 48 h 0.4M NaCl"

/dev\_stage="Six week old"

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI"

BASE COUNT 202 a 214 c 188 g 211 t

ORIGIN

Query Match

57.8%; Score 393.4; DB 9; Length 815;

Best Local Similarity 75.9%; Pred. No. 7.5e-109;

Matches 512; Conservative 0; Mismatches 161; Indels 2; Gaps 2;

7 GGTGGCTGGCAGAGGGCCAGCCCTTTATGATGGTGGTGGATCGGCACATG 66

105 GGTGGTGGTGTATGCTCATGACCATTTTACGGTGGAGGGAGCGCTCGGACATATG 164

67 GGTGGAGCTGGGTATGGGAATTTATACAGCCAGAGGATAGGACAGACAGCGTGGC 126

165 GGGGGTGTGTGGATACGGAACCTGTACAGCCAGAGGATAGGACAGCGTGGC 224

127 CTGAGCACTGGGCTATTATACATGATGATGATGATGATGATGATGATGATGATG 186

225 TTTAGACAGGCGCTCTTCAATACGAGGTTGAGCTGAGCTGCTATGAAATGAAATGT 284

187 ACAACAGACCTTAATGGTGGCTTCGAGGACATATTAGGCTCACTGGCACCACCTTTGC 246

285 AACAGACAGCCCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 344

247 CCTGCTTAATCTTGGCTCTTCAACACATGATGATGATGATGATGATGATGATGATG 306

345 CCACCTTAATCTTGGCTCTTCAACACATGATGATGATGATGATGATGATGATGATG 404

307 TTGACATGGTGGAGCGCTTCCTTCAATGCTCAATGCTCAATGCTCAATGCTCAATG 366

405 TTTGACATGGTGGAGCGCTTCCTTCAATGCTCAATGCTCAATGCTCAATGCTCAATG 464

367 GTCTCTTCTTAGAGTACATGATGATGATGATGATGATGATGATGATGATGATGATG 426

465 ATTGCTTCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 524

427 CACTCATCTTCAACCTGCTTCAACACATGATGATGATGATGATGATGATGATGATG 486

525 CACTCTTCAACCTGCTTCAACACATGATGATGATGATGATGATGATGATGATGATG 584

487 GTGTCGATGAAGGGGTCTGCACTGATGATGATGATGATGATGATGATGATGATG 546

585 GTGTCGATGAAGGGGTCTGCACTGATGATGATGATGATGATGATGATGATGATG 644

547 TGGCAAGACCAACATATCTCAATGGCCAGAGCGCTTCTTCAAGTCACTTCAAGTAT 606

645 TGGCAAGACCAACATATCTCAATGGCCAGAGCGCTTCTTCAAGTCACTTCAAGTAT 703

607 GGTGCACTCTCACTGCTATATATCTGCTTCAATGGCCAGAGCGCTTCTTCAAGTAT 666

704 CGAGGAGACCTGAGCTAGC-ACAACATGTTCTGCTCATTTGGGACACATTTT 762

667 GAAGGCTCTCAATTC 681

763 GTGGGTTGGCAATTC 777

RESULT 5

BG446553

LOCUS

BG446553

DEFINITION

GA\_Eb0035J13f Gossypium arboreum 7-10 dpa fiber library Gossypium

ACCESSION

BG446553

VERSION

BG446553

KEYWORDS

EST.

SOURCE

Gossypium arboreum.

ORGANISM

Gossypium arboreum

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE

Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

JOURNAL

1 (bases 1 to 868)

COMMENT

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry

of the cotton fiber

An integrated analysis of the genetics, development, and evolution

Unpublished (2000)

Contact: Wing, R.A.

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TATACACTCTCATATAGG

High quality sequence stop: 843.

Location/Qualifiers

1. 868

/organism="Gossypium arboreum"

/strain="AKA"

/cultivar="8400"

/db\_xref="taxon:29729"

/clone="GA\_Eb0035J13f"

/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue\_type="Fibers isolated from bolls harvested 7-10

dpa"

/lab\_host="E. coli"

/note="Vector: pBR-CMV; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 239 a 189 c 216 g 224 t

ORIGIN

Query Match

56.4%; Score 384; DB 10; Length 868;

Best Local Similarity 72.8%; Pred. No. 5.8e-106;

Matches 495; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

1 GACTAGGTGGCTGGCAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGTGGC 60

13 GACAATGGTGGTGGCAGAGCGGCGACGACCTTTATGATGGTGGTGGTGGTGGC 72

61 ACCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120

73 ACAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 132

121 GTGGCGTGGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180

133 GCACTTTGAGCCTGCTCACTTTCAACAATGGCTGGAGTGGGCTGCTGCTGAGCTC 192

181 ACTTGTACAAAGCAGCCCTTAATGCTTCCGGAACATTAAGGCTCACTGCCACCAAC 240

193 CGGTGACAAATATCTCTCATGCTGCTTATGACGACCATTAACGCTGACGACCAAC 252

241 TTTTGGCTCTCACTTCTCTCTCTCAACAATGATGATGATGATGATGATGATGATG 300

253 TTTTGGCTCTCACTTCTCTCTCTCAACAATGATGATGATGATGATGATGATGATG 312

301 CAACACTTGGACATGCTGATGCTGCTTCAACAATGATGATGATGATGATGATGATG 360

313 GAACACTTGGATTTGGCCAGACCGGCTCTTCAACAATGATGATGATGATGATGATG 372

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OY	421	AATGGCCACTCATCTACTTCAACCTCGTTTTGATCACAACGTCGGTGGGACAGGCAGTC	480
Db	433	AATGACACTTCTCTACTTCAACATGTGCGATTTGAATACGAACGTGGGAGTGCACGAGGATATA	492
OY	481	CACCTGTGTGCGATTAAGGGGCTCGAAGCTGGATGGCAATCCCATGCTCTGAATTTGGGC	540
Db	493	ACGTAGTGTCCATCAAGGCTTCACGAAAGAGATGGTACATGTATCCAGAAATTTGGGCG	552
OY	541	CAAAACGTGGCAAGCAACACTATCTCAATGGCCAAAGCCTTTCCTTCAAGTCACTCTT	600
Db	553	CAAAACCTGGCAAGCAAACTTACCTTAAACGCAAAAGCCTCTCTTTTAAATGACTGCC	612
OY	601	AGTGAAGTGCAGCTCTACTCTATATATCTCGTTCCCTCCCAATGGCAATTTGGCA	660
Db	613	AGCGATGGCAGGACTATTAACAGCTTACAATGTATGTCCGTGCGTTGGCAATTTGGACAA	672
OY	661	ACCTATGAAGGCCCTTCATTT	680
Db	673	ACTTTTGAAGCAAGCCAACT	692

RESULT	LOCUS	DEFINITION	966 bp	mRNA	linear	EST
6	BE055631	GA__E0003JJ22f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum CDNA clone GA__E0003JJ22f, mRNA sequence.				07-MAR-2001

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VERSION ..... BE055631.2  GI:13245739
KEYWORDS .....
SOURCE .....
      Gossypium arboreum,
      EST.

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ORGANISM  
Gossypium arboreum  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.  
1 (bases 1 to 966)  
Wing, R.A., Fleisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry

**TITLE** An integrated analysis of the genetics, development, and evolution of the cotton fiber

**JOURNAL** Unpublished (2000)

**COMMENT** On Jun 8, 2000 this sequence version replaced gi:8382688.

Contact: Mike R.

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: [twing@clemson.edu](mailto:twing@clemson.edu)  
Seq primer: TAATTCAGCTCCTATTCAGG  
High quality sequence start: 4  
High quality sequence stop: 945.

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SOURCE
1. 966
/organism="Gossypium arboreum"
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dpa"
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ORIGIN

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Query Match	56.1%;	Score 382;	DB 9;	Length 966;
Best Local Similarity	73.0%;	Pred. NO. 2.5e-105;		
Matches 490; Conservative	0;	Mismatches 181;	Indels 0;	Gaps 0;

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QY	241	TTT	TG	CC	CT	CT	TA	CT	TG	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	300
		1111	1	1	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	
Db	276	TTT	TG	CC	CA	CT	TA	CT	TG	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	335
		1111	1	1	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	
QY	301	CAA	C	AT	TG	CA	T	G	CA	T	G	CA	T	G	CA	T	G	CA	T	G	360
		111111	1	1111	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
Db	336	GAA	C	AT	T	G	CA	T	G	CA	T	G	CA	T	G	CA	T	G	CA	T	395
		111111	1	1111	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
QY	361	GT	CC	CC	CG	T	CT	CT	TG	T	AG	GT	T	AC	CA	T	GT	A	GA	AA	420
		1111	1	1	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	1111	
Db	396	GT	CC	CC	CG	T	AT	TG	T	CA	GA	GT	T	AC	CA	T	GT</				

RESULT 7	BE034856	LOCUS	DEFINITION	ACCESSION
	BE034856	775 bp	mRNA	linear
	ML050C12	ML Mesembryanthemum crystallinum	CDNA 5'	mRNA sequence.
	BE034856			

KEYWORDS	EST.
KEYWORDS	EST.
SOURCE	Common ice plant.
ORGANISM	Mesembryanthemum crystallinum
AUTHORS	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Caryophyllidae: Caryophyllales: Alzooceae: Mesembryanthemum.
REFERENCE	1 (bases 1 to 775)
AUTHORS	Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferreira,H., Kwasniski,S., McCollough,A., Michalowski,C.B., Palacios,C., Scara,G., Wheeler,M. and Zepeda,G.R.
TITLE	Functional Genomics of Plant Stress Tolerance
JOURNAL	Unpublished (2000)
COMMENT	Contact: Michalowski,C.B.

BIO SCIENCES WEST ROOM 513, TUCSON, AZ 85721, USA  
 Tel: 520-621-7982  
 Fax: 520-621-1697



Db 519 TTCTATTTTCCTTCAGAAAGTCCCTGTGTGAAGAAAGAGATCATTCACATTA 578  
 Oy 422 ATGGCACTCATCTCACTCAACCTCTGTTTGTATCACAACCTGCGGCGAGCGAGCTCC 481  
 Db 579 ATGACACATCATCTCACTCAACCTGTTTGTATCACAACCTGCGGAGATGTAC 638  
 Oy 482 ACTCTGTGTATGAAGGGTCTCGAAGCTGATGCGCATCTCTTACAAATTTGGGGCC 541  
 Db 639 ATTCTGTGTATCAAGGGTCTCGAAGCTGATGCGCATCTCTTACAAATTTGGGGCC 698  
 Oy 542 AAAAGCTGCAACCAACTATCTCAAGCTGATGCGCATCTCTTACAAATTTGGGGCC 584  
 Db 699 AGAAGCTGCAACCAACTATCTCAAGCTGATGCGCATCTCTTACAAATTTGGGGCC 740  
 RESULT 9  
 BFA79593 706 bp mRNA linear EST 20-FEB-2001  
 LOCUS L48-3281T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours  
 DEFINITION Nac1 treatment Mesembryanthemum crystallinum cDNA clone L48-3281  
 5', mRNA sequence.  
 ACCESSION BFA79593.1 GI:11550420  
 VERSION BFA79593  
 KEYWORDS EST.  
 SOURCE common ice plant.  
 ORGANISM Mesembryanthemum crystallinum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Caryophyllaceae; Mesembryanthemum.  
 REFERENCE 1 (bases 1 to 706)  
 Cushman, J.C.  
 An expressed sequence tag database for the common ice plant,  
 Mesembryanthemum crystallinum  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Cushman JC  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T7  
 BACKWARD: T3  
 Plate: L48-33 row: G column: 9  
 Seq primer: T3  
 High quality sequence stop: 350  
 POLYA-No.  
 FEATURES  
 location/Qualifiers  
 source 1..706  
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 /db\_xref="taxon:3544"  
 /clone="L48-3281"  
 /clone\_id="Ice plant Lambda Uni-Zap XR expression library  
 /48 hours Nac1 treatment"  
 /issue-type="leaf, 48 h 0.4M NaCl"  
 /dev-stage="six week old"  
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 BASE COUNT 187 a 176 c 162 g 181 t  
 ORIGIN  
 Query Match 53.7%; Score 365.6; DB 10; Length 706;  
 Best Local Similarity 76.4%; Pred. No. 2.1e-100;  
 Matches 449; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
 Oy 94 TACAGCAAGGATATGACGACGAGGATGCGCTGACGACATGCTATTAAACAAATGA 153  
 Db 2 TACAGCAAGGATATGACGACGAGGATGCGCTGACGACATGCTATTAAACAAATGA 61  
 Oy 154 TTAAGTGTGTGCTTCTGCAATGACTTGTACAAAGACCCCTTAATGGCTTCGG 213

Db 62 TTGAGCTGTGAGGCTTGCTATGAATGAATGAATGAATGAATGAATGAATGAATGA 121  
 Oy 214 GGAAGCTATTAAGGCTACCTGCGACCAACCTTTGGCTCTTACCTTTGGCTCTTACCAAC 273  
 Db 122 GGAAGCTATTAAGGCTACCTGCGACCAACCTTTGGCTCTTACCTTTGGCTCTTACCAAC 181  
 Oy 274 AATGCTGTGATGCGCAACCTCTCTCTCCACCACTTGCACATGAGTGGAGCCCTTCCTT 333  
 Db 182 AATGCTGTGATGCGCAACCTCTCTCTCCACCACTTGCACATGAGTGGAGCCCTTCCTT 241  
 Oy 334 CAATGCTCAATTAACGAGCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 393  
 Db 242 AAGATTTGCCCAATTAACGAGCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 301  
 Oy 394 AAGAAAGTGGAGTGAATTAAGGCTTACATCAATGAGGCTCAATCAATCAATCAATCAAT 453  
 Db 302 AAGAAAGTGGAGTGAATTAAGGCTTACATCAATGAGGCTCAATCAATCAATCAATCAAT 361  
 Oy 454 ACAAGCTGTGAGGCTGCGGACGAGCTGCGACCTGCTGTGTGATTAAGGGGTCTGCAACTGGA 513  
 Db 362 TCCAAAGTGTGAGGCTGCGGACGAGCTGCGACCTGCTGTGTGATTAAGGGGTCTGCAACTGGA 421  
 Oy 514 TGGCAATCATCTCTTGAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATCTCAATTC 573  
 Db 422 TGGCAATCATCTCTTGAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATCTCAATTC 481  
 Oy 574 CAAGGCTCTTCTCTTCAAGTCACTCTTGAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATTC 633  
 Db 482 CAAGGCTCTTCTCTTCAAGTCACTCTTGAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATTC 541  
 Oy 634 GTTCTCTTCAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATCTCAATTC 681  
 Db 542 GTTCTCTTCAATTAAGGGGTGCGGACCAACCTGCGAAGCAACCAATCTCAATTC 589  
 RESULT 10  
 AM776306 668 bp mRNA linear EST 07-SEP-2000  
 LOCUS EST335371 DSIL Medicago truncatula cDNA clone pDSIL-7M2, mRNA  
 DEFINITION sequence.  
 ACCESSION AM776306  
 VERSION AM776306  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 REFERENCE 1 (bases 1 to 668)  
 Fedorova, M., Peterson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng  
 H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S.,  
 Holt, I.E., and Fraser, C.M.  
 ESTs from leaves of Medicago truncatula after inoculation with  
 Colletotrichum trifolii  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Deborah A. Samac  
 Department of Plant Pathology  
 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
 Tel: 612 625 1243  
 Fax: 612 649 5058  
 Email: debby@puccini.crl.umn.edu  
 Minnesota sequence name: M256339e  
 TIGR sequence name: MTFAR737K  
 More information is available at:  
 http://chrysis.tamu.edu/medicago  
 Seq primer: Skmod (CTA GAA CTA gtg gat CC).  
 FEATURES  
 source 1..668  
 /organism="Medicago truncatula"  
 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"

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/clone="pDSIL-7M2"
/tissue_type="leaves infected with Colletotrichum
trifolii"
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
BASE COUNT      181 a      118 c      156 g      213 t
ORIGIN

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Query Match      52.8%; Score 359.4; DB 9; Length 668;
Best Local Similarity 78.1%; Pred. No. 1.6e-98;
Matches 432; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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```

QY 1 GACTACGCTGGCTGGGAGAGCGGCGACGCTTTATGCTGGTGACGATCGGC 60
DB 116 GATTATGCTGGTGGAGAGTGGTATGCTTCTATGCTGGTGATGCTTCTGCG 175
QY 61 ACCATGGGTGAGCTGGTGGTATGGAATTTATACGCGAGGATGAGCGAGACAG 120
DB 176 ACAATGGGTGAGCGATGCTGATGATGAAATTTATAGCCAGAGATATGAAACACACACA 235
QY 121 GTGGCGCTGAGCGCTGCTATTTAAATGATTAAGTTGCTGCTTCTGCAATG 180
DB 236 GCGAGCTAGGACGCTCTTGTTCACAAATGTTAAAGCTGATGATGATGAATG 295
QY 181 ACTTGTACAAAGACGCTTAAATGCTGCTCCGGAACATTAAGGCTCAGCCACAC 240
DB 296 AGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 355
QY 241 TTTTGGCTGCTTAACTTCTCTCCCTTAAACAAATGATGATGATGATGATGAT 300
DB 356 TTTTGGCTGCTTAACTTCTCTCCCTTAAACAAATGATGATGATGATGATGAT 415
QY 301 CAACACTTGGACATGCTGCTGCTGCTTCAATGCTCAATACCGAGCTGATTC 360
DB 416 CAACACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 361 GTCCCGCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 476 GTGCTGCTTCTTGAAGAGGTGATGATGATGATGATGATGATGATGATGAT 535
QY 421 AATGCGCATCTACTTCACTCTGTTTGAATCAAAAGTGGGCGAGCGAGCTC 480
DB 536 AATGCGCATCTACTTCACTCTGTTTGAATCAAAAGTGGGCGAGCGAGCTC 595
QY 481 CACTGTGCTGATTAAGAGGTCTGCAATGATGATGATGATGATGATGATGAT 540
DB 596 CATTCTATATCATCAAAAGGTCAAAAGTGGATGATGATGATGATGATGATGAT 655
QY 541 CAAAACCTGGCAAA 553
DB 656 CAAAATTTGGCAAA 668

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```

RESULT 11
LOCUS      BE584282
DEFINITION 7-3E-HA PsjoeHa glycine max/Phytophthora sojae mixed EST library
ACCESSION BE584282
VERSION    BE584282.1 GI:9835231
KEYWORDS   EST.

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SOURCE      Glycine max/Phytophthora sojae mixed EST library.
ORGANISM    Glycine max/Phytophthora sojae mixed EST library
REFERENCE    1 (bases 1 to 654)
AUTHORS      Qutob,D., Hraber,P.T., Sobral,B.W.S. and Gijzen,M.
TITLE        Comparative analysis of expressed sequences in Phytophthora sojae
JOURNAL      Plant Physiol. 123 (1), 243-254 (2000)
MEDLINE      20267956
COMMENT      Contact: Gijzen M
              Agriculture and Agri-Food Canada
              1391 Sandford Street, London, Ontario, Canada N5V 4T3
              Tel: 519 457 1470
              Fax: 519 457 3997
              Email: gijzenm@agr.ca
              Transcript obtained from mixed plant-pathogen interaction culture.

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FEATURES
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        1..654
            /organism="Glycine max/Phytophthora sojae mixed EST
            library"
            /strain="Phytophthora sojae race 2 strain P6497"
            /cultivar="Glycine max cultivar Harosoy"
            /db_xref="taxon:135715"
            /clone_id="PsojoeHa"
            /tissue_type="Plant hypocotyls infected with Phytophthora
            sojae"
            /dev_stage="8 d old etiolated hypocotyls 48 h
            post-inoculation with Phytophthora sojae zoospores"
            /lab_host="E. coli strain XLOLR"
            /notes="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This
            cDNA library was constructed from polyA+ enriched mRNA
            from etiolated hypocotyls 48 h post-inoculation with
            Phytophthora sojae zoospores. Complementary DNA was
            synthesized from mRNA using an XhoI-poly(dT)
            linker-primer. EcoRI adapters were ligated to the
            blunt-ended cDNA fragments and the products were digested
            with XhoI for directional cloning into lambda ZAP Express
            vector. This lambda library was amplified once using E.
            coli host strain XL1 Blue MRF+. Inserts were then
            subcloned by mass excision using EXSist helper phage
            for conversion into phagemid vector pBK-CMV in E. coli
            host strain XLOLR. Sequenced using T3 primer: 5' ATT AAC
            CCT CAC TAA AGG GA 3'."

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```

BASE COUNT      172 a      150 c      148 g      184 t
ORIGIN

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Query Match      52.7%; Score 358.6; DB 10; Length 654;
Best Local Similarity 76.6%; Pred. No. 2.7e-98;
Matches 439; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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QY 109 GGCAGAACACGCTGGGCTGAGCAGCTGCGCTATTAAACAAATGATGATGAT 168
DB 1 GGAACCAACACTGCGACATGACAGCTGCTCTATTAAACAAATGATGATGATGAT 60
QY 169 TGTCTGAATGACTTGTACAAAGCAATGATGATGATGATGATGATGATGAT 228
DB 61 TGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 229 ACTGCGACCAACTTTGCTCTTAACTTGTGCTCCCTTAAACAAATGATGATGAT 288
DB 121 ACTGCGACCAACTTTGCTCTTAACTTGTGCTCCCTTAAACAAATGATGATGAT 180
QY 289 AACCTCTCTCCAACTTGCAGATGCTGAGCTGCTCTTCAAAATGCTCAATAC 348
DB 181 AACCTCTCTTGAACACTTGCAGATGCTGAGCTGCTCTTCAAAATGCTCAATAC 240
QY 349 CGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
DB 241 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 409 AGTTTAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
DB 301 AGTTTAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

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FEATURES	Seq primer: T3.	Location/Qualifiers
Source	1..710	
		/organism="Lycopersicon esculentum"
		/cultivar="TA496"
		/db_xref="taxon:4081"
		/clone="CLOC18N14"
		/clone_1lb="LomaTo flower, 8 mm to preanthesis buds"
		/tissue_type="flower"
		/dev_stage="buds 8mm to preanthesis"
		/note="Vector: Bluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
BASE COUNT	187 a	143 c 147 g 233 t
ORIGIN		
Query Match	52.3%;	Score 356; DB 10; Length 710;
Best Local Similarity	75.2%;	Pred. No. 1.8e-97;
Matches 457; Conservative	0;	Mismatches 150; Indels 1; Gaps 1;
OY	1	GACTACGCTGCTGCGACAGCGCCACGCCACCTTTATGCTGCTGCTGCGATCGCATCGGC 60
DB	100	GATTATGCGAGATGCGCAACATGCTCATCCACTTCTATGAGGAGGCGATGCTCTGGC 139
OY	61	ACCATGGGGGAGCGCTTGGGGGATGAGAAATTATACAGCCAGAGGATATGCGACAGACG 120
DB	160	ACAATGGGGGGGCTCTTGCGATATGGAATTTGTTATACCAAGGGATGAGAACTACACT 219
OY	121	GTGGCGCTGAGCAGTGGCGCTATTTAACAATGAGATTAACTGTGTGCTGCTTGCAGATG 180
DB	220	GCAGCAGTAAGTACAGCACTATTCAACAATGGTTTAACTTGGTGCTTGTATGAGCTC 279
OY	181	ACTGTACAAAGACCCATAATGGGCGCTCCGGGAACTATTAGGCTACATGCCACCAAC 240
DB	280	ACTTGACAAATGACACTAATGAGTGTCTCCAGGAGCACTATTACGTACAGCAACTAAT 339
OY	241	TTTTGGCCCTCTAATCTTGTGCTCTCCCTAACACAACAATGGTGATGGTCACACCTCTC 300
DB	340	TTTTTGCTCCGACCCGCTCTACCTAACAATATGGTGGTGGTGCAATCCCTCTC 399
OY	301	CAACACTTGCACATGGCTAGCGCTGCTCCCTTCAATGGCTCATTCAGAGCTGATC 360
DB	400	CAACATTTGATTTACACACACCTGTTCTTGCAATTTGCTAAATTAACAACCGGATAC 459
OY	361	GTCCCGCTCTCTTTGTAGGATCAGATATGAAAGAAGTGAAGTGAAGTTTACAATC 420
DB	460	GTCCCTGATCTTTTGGAAGGGGCGCCCTGTATGAAAGAAGGAGAAATTAAGTTTACAGTA 519
OY	421	AATGGCCACTCATCTCAACCTCGTTTGAATCACAAGCTGGGTGGCGCAGGCACTC 480
DB	520	AATGACACACTATTTTCAACTGGTTTATGAGCAAAATGGTGAAGTGGTGTATAT 579
OY	481	CACCTGTGTCATTAAGGGGCTCGACAGTGGATGCAATTCATGCTAGAAATTTGGGCG 540
DB	580	TCATCACTTTCATTTA-GGGTCTAATACTGATGGCAAGCATATCAAGAAATTTGGGCG 638
OY	541	CAAACTGGCAAGCAACAATCTCAATGAGCCAAAGGCTTTCTTCAATCACTCTT 600
DB	639	CAAAATTTGGCAAGCAATCTTAATCAATGTCAAAGTCTTCAATTTCACTGACACACA 698
OY	601	AGTATGG 608
DB	699	AGTATGG 706
RESULT 14		
LOCUS	AW584547	695 bp mRNA linear EST 07-SEP-2000
AW584547		
DEFINITION	n210609e MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone MHAM-2F17, mRNA sequence.	

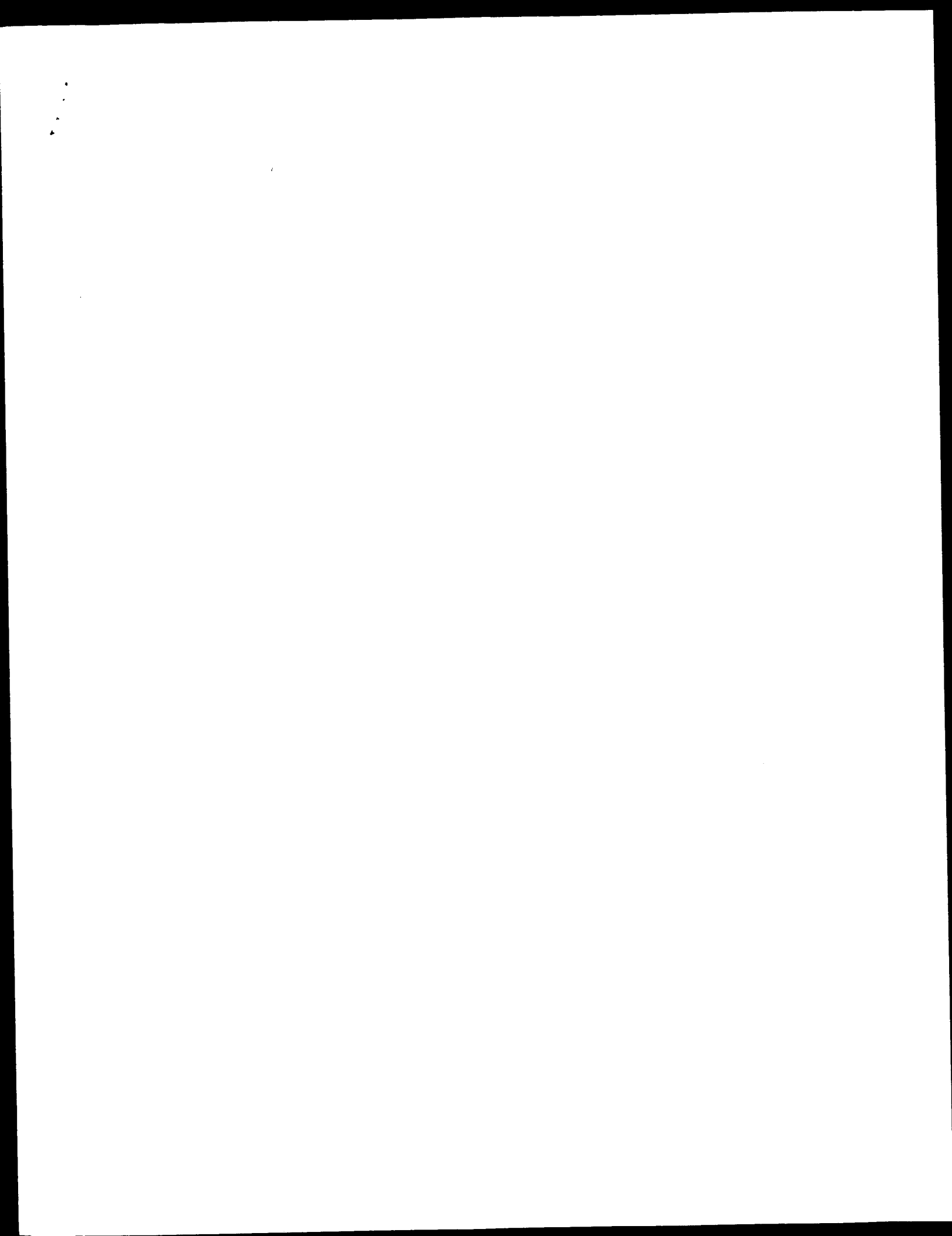
ACCESSION	AM584547	GI:7261601
VERSION	EST.	
KEYWORDS	Medicago truncatula/Glomus versiforme mixed EST library.	
SOURCE	Medicago truncatula/Glomus versiforme mixed EST library	
ORGANISM	Eukaryota; mixed EST libraries.	
REFERENCE	1 (bases 1 to 695)	
AUTHORS	Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D., Bowman,C.L., Craeven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.	
TITLE	ESTs from roots of Medicago truncatula after colonization with Glomus versiforme	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Harrison M.J. Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73401 Tel: 580-223-5810 Fax: 580-221-7380 Email: mjharrison@noble.org Other name: MHAM-zc-c09; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrystle.tamu.edu/medicago'.	
FEATURES	Seq primer: T3.	
SOURCE	Location/Qualifiers	
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	/organism="Medicago truncatula/Glomus versiforme mixed EST library"	
	/cultivar="Medicago truncatula genotype A17"	
	/db_xref="taxon:119092"	
	/clone="MHAM-2P17"	
	/tissue_lib="MHAM"	
	/tissue_type="roots colonized with Glomus versiforme"	
	/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."	
	/lab_host="E. coli strain XLOLR"	
	/note="Vector: pBluescript SK-. Site-1: EcoRI. Site-2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."	
BASE COUNT	185 a 150 c 156 g 204 t	
ORIGIN		
Query Match	52.0%; Score 353.8; Db 9; Length 695;	
Best local similarity	78.4%; Pred. No. 8.3e-97;	
Matches 424; Conservative	0; Mismatches 117; Indels 0; Gaps 0	
QY	7 GGGGGGTGGCAGAGGGCCACCTTTATGTTGGTGAGCAGCATGTGGACCATG 66	
Db	155 GGTGATGGGAAATATGCCATGCCACATTTTATGTTGGAGAGATCATCAGCAATG 214	
QY	67 GGTGAGCTTGTGGTATGGGAATTTATACGCCAAGGGTATGGCAGCAACGGTGGG 126	
Db	215 GGAGGGGGTGTGGTTATGAAATTTGATAGCCAAAGCGATATGGAACCAACCTCGA 274	
QY	127 CTGAGACCTGGCCTATTTAACAATGAGATTAGTTGGTGTCTTCTTCAAAATGACTTG 186	
Db	275 CTTAGACATGCTCTTTTACAACAATGAGATTGAGTTGGTGGCTTGTCACGAGTGAATGT 334	
QY	187 ACAAAAGACCTTAATGTGCTTCGGGACATAATAGGGTCACTGCACCAACTTTTGC 246	
Db	335 AAGAGTACCTTAATATGAGCTTCCTGTTAGCATATTTGTTACTGCTCAACAACTTGC 394	
QY	247 CCTCTAATCTTGCTCTCCCTTAACAACAATGGTGGATGGCAACCTCCTCTCCACAC 306	
Db	395 CCCCCAAACTTTGCAAGAGCTAATATCAACATGTTGGATGGTCAACCTCTCCCTTCAGCAC 454	
QY	307 TTGACATGAGCTGAGGCTCTCTCTTCAAAATCCCTCAATACGAGAGTGATGTCGCC 366	

Query Match	52.0%	Score 353.8;	DB 9;	Length 702;
Best Local Similarity	76.6%	Pred. No. 8.3e-97;		
Matches 433;	Conservative 0;	Mismatches 132;	Indels 0;	Gaps 0;

2	ACTACGCTGCTGSCAGAGCGGCGACGCCACCTTTATATGCTGCTGCTGACGCATCTTGCA	61

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Search completed: October 14, 2002, 00:08:00
Job time : 1952 secs
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2002, 18:25:39 : Search time 80 seconds  
(without alignments)  
2090.955 Million cell updates/sec

Title: US-09-896-301-1

Perfect score: 681  
Sequence: 1 gactacggtgctgctgcagag.....cctatgaagccctcaattc 681

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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3: /cgn2\_6/ptodata/2/lna/5B.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/lna/6A.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/lna/6B.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/lna/6C.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	100.0	681	2	US-08-440-517A-1
2	681	100.0	681	4	US-09-092-160-1
3	276.4	40.6	537	2	US-08-845-539-5
4	276.4	40.6	537	4	US-09-362-642-5
5	259.4	38.1	727	1	US-07-885-970A-6
6	259.4	38.1	727	1	US-08-298-687A-6
7	259.4	38.1	727	1	US-08-530-797-5
8	259.4	38.1	727	1	US-08-298-829-6
9	259.4	38.1	727	2	US-08-787-335-5
10	253.4	37.2	2415	1	US-07-885-970A-26
11	253.4	37.2	2415	1	US-08-298-687A-26
12	253.4	37.2	2415	1	US-08-298-829-26
13	251.6	36.9	702	2	US-08-845-539-1
14	251.6	36.9	702	4	US-09-362-642-1
15	242.8	35.7	501	2	US-08-845-539-3
16	242.8	35.7	501	4	US-09-362-642-3
17	31.8	4.7	1685	1	US-08-486-721A-1
18	31.8	4.7	7218	1	US-08-232-463-14
19	30.2	4.4	3771	1	US-07-876-280-5
20	30.2	4.4	3771	1	US-08-049-783-1
21	30.2	4.4	3771	1	US-08-158-232-5
22	30.2	4.4	3771	1	US-08-304-626-5
23	30.2	4.4	3771	1	US-08-316-301A-5
24	30.2	4.4	3771	1	US-08-611-928-5
25	30.2	4.4	3771	3	US-09-173-891-5
26	30.2	4.4	3771	4	US-09-076-137-5
27	30.2	4.4	3771	5	PCT-US92-03624-5

C	28	29.6	4.3	1869	4	US-09-350-268-1	Sequence 1, Appl
C	29	29.4	4.3	2184	3	US-08-755-587-170	Sequence 170, App
C	30	28.8	4.2	1318	4	US-08-986-304-1	Sequence 1, Appl
C	31	28.8	4.2	1443	4	US-09-160-119-3	Sequence 3, Appl
C	32	28.8	4.2	2095	4	US-09-160-119-1	Sequence 1, Appl
C	33	28.8	4.2	11561	1	US-08-450-332-1	Sequence 1, Appl
C	34	28.8	4.2	11561	2	US-08-637-640-1	Sequence 1, Appl
C	35	28.8	4.2	11561	4	US-09-004-406C-1	Sequence 1, Appl
C	36	28.6	4.2	4758	3	US-09-191-647-1	Sequence 1, Appl
C	37	28.6	4.2	4758	4	US-09-245A-1	Sequence 1, Appl
C	38	28.6	4.2	4758	4	US-09-340-153-1	Sequence 1, Appl
C	39	28.6	4.2	90050	4	US-09-245-041-5	Sequence 5, Appl
C	40	28.6	4.2	4411529	4	US-09-103-840A-1	Sequence 1, Appl
C	41	28.4	4.2	648	4	US-08-998-416-111	Sequence 111, App
C	42	28	4.1	954	2	US-08-973-275-2	Sequence 2, Appl
C	43	27.8	4.1	1233	3	US-08-718-904-80	Sequence 80, Appl
C	44	27.8	4.1	2574	4	US-09-142-529-2	Sequence 2, Appl
C	45	27.6	4.1	595	2	US-08-231-193A-17	Sequence 17, Appl

## ALIGNMENTS

```
RESULT 1
US-08-440-517A-1
; Sequence 1, Application US/08440517A
; Patent No. 5959082
; GENERAL INFORMATION:
; APPLICANT: COSGROVE, DANIEL J.;
; APPLICANT: GUILTINAN, MARK;
; APPLICANT: SCHERBAN, TATYANA;
; APPLICANT: SHI, JUN
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
; ADDRESS: PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY PARK
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440.517A
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; US-08-440-517A-1

Query Match 100.0%; Score 681; DB 2; Length 681;
Best Local Similarity 100.0%; Pred. No. 1.3e+228;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTACGGTGGCTGCGAGAGCGGCGACGACCTTTATGTTGGTGGTACCATCTGAC 60
Db 1 GACTACGGTGGCTGCGAGAGCGGCGACGACCTTTATGTTGGTGGTACCATCTGAC 60
QY 61 ACCATGGGTGAGACCTGTTGGGTATGGGAATTATACAGCCAGAGGTATGGACGAGAC 120
Db 61 ACCATGGGTGAGACCTGTTGGGTATGGGAATTATACAGCCAGAGGTATGGACGAGAC 120
QY 121 GTGGCGCTGAGCACTGCGCTATTTACATGATTTAGTTGTGGTCTTCTTCGAATG 180
Db 121 GTGGCGCTGAGCACTGCGCTATTTACATGATTTAGTTGTGGTCTTCTTCGAATG 180
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Db 121 GTGGCGCTGAGCACTGGCGCTATTAAACATGATTAAGTTGTGTGCTGCTTGCATGATG 180  
QY 181 ACTGTGAACAAAGCAACCTTAATGTGCTTCCGGGAACTATTAGGCTCATGCTCCACCAAC 240  
Db 181 ACTGTGAACAAAGCAACCTTAATGTGCTTCCGGGAACTATTAGGCTCATGCTCCACCAAC 240  
QY 241 TTTTGCCCTCTAACTTGTCTCTCCCTAACAAAGTGGATGGTCAACCCCTCTCTC 300  
Db 241 TTTTGCCCTCTAACTTGTCTCTCCCTAACAAAGTGGATGGTCAACCCCTCTCTC 300  
QY 301 CAACACTTGCAGATGCTGAGCTGAGCTTCTTCAATTCGCTCAATACCGAGCTGTATC 360  
Db 301 CAACACTTGCAGATGCTGAGCTGAGCTTCTTCAATTCGCTCAATACCGAGCTGTATC 360  
QY 361 GTCCCGCTCTCTTGTGTAAGGCTGATGATGAAGAAAGTGGAGTGTATACATC 420  
Db 361 GTCCCGCTCTCTTGTGTAAGGCTGATGATGAAGAAAGTGGAGTGTATACATC 420  
QY 421 AATGGCCACTCATCTTCAACCTGTTTGTATCACAACCTGGTGGCGAGCGAGCTC 480  
Db 421 AATGGCCACTCATCTTCAACCTGTTTGTATCACAACCTGGTGGCGAGCGAGCTC 480  
QY 481 CACTCTGTGTGATGAAGGGGTCTCGAAGTGGATGGCAATTCATGTAGAAATTTGGGGC 540  
Db 481 CACTCTGTGTGATGAAGGGGTCTCGAAGTGGATGGCAATTCATGTAGAAATTTGGGGC 540  
QY 541 CAAAACTGGCAAGCAACACTATCTCATGAGGCAAGGCTTCTTCAAGTCACTCTT 600  
Db 541 CAAAACTGGCAAGCAACACTATCTCATGAGGCAAGGCTTCTTCAAGTCACTCTT 600  
QY 601 AGTATGTGTGCACTGCTCATATATCTGTTCTTCAATTTGGCAATTTGGCCAA 660  
Db 601 AGTATGTGTGCACTGCTCATATATCTGTTCTTCAATTTGGCAATTTGGCCAA 660  
QY 661 ACCTATGAAGGCTCTCAATTC 681  
Db 661 ACCTATGAAGGCTCTCAATTC 681

## RESULT 2

US-09-092-160-1

; Sequence 1, Application US/09092160C  
; Patent No. 6235466  
; GENERAL INFORMATION:  
; APPLICANT: Cosgrove, Daniel J  
; APPLICANT: McQueen-Mason, Simon  
; APPLICANT: Guillinan, Mark J  
; APPLICANT: Shepherdan, Tatyana  
; APPLICANT: Shi, Jun  
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS  
; FILE REFERENCE: 1194/1C114US3  
; CURRENT APPLICATION NUMBER: US/09/092,160C  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 08/440,517  
; EARLIER FILING DATE: 1995-05-12  
; EARLIER APPLICATION NUMBER: 08/242,090  
; EARLIER FILING DATE: 1994-05-12  
; EARLIER APPLICATION NUMBER: 08/060,944  
; EARLIER FILING DATE: 1993-05-12  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 681  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber  
; OTHER INFORMATION: expansin  
US-09-092-160-1

Query Match 100.0%; Score 681; DB 4; Length 681;  
Best local Similarity 100.0%; Pred. No. 1.3e+28;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGGCTGGCTGGAGAGCGGCCACGCCACTTTTATGCTGTGTGTACCATCTGGC 60  
Db 1 GACTAGGCTGGCTGGAGAGCGGCCACGCCACTTTTATGCTGTGTGTACCATCTGGC 60  
QY 61 ACCATGGGTGAGCTGTGTGGTATGGGATTTATACAGCAAGGGTATGAGCGACAGC 120  
Db 61 ACCATGGGTGAGCTGTGTGGTATGGGATTTATACAGCAAGGGTATGAGCGACAGC 120  
QY 121 GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGTGTGCTTGTGAAATG 180  
Db 121 GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGTGTGCTTGTGAAATG 180  
QY 181 ACTGTGAACAAAGCAACCTTAATGTGCTTCCGGGAACTATTAGGCTCATGCTCCACCAAC 240  
Db 181 ACTGTGAACAAAGCAACCTTAATGTGCTTCCGGGAACTATTAGGCTCATGCTCCACCAAC 240  
QY 241 TTTTGCCCTCTAACTTGTCTCTCCCTAACAAAGTGGATGGTCAACCCCTCTCTC 300  
Db 241 TTTTGCCCTCTAACTTGTCTCTCCCTAACAAAGTGGATGGTCAACCCCTCTCTC 300  
QY 301 CAACACTTGCAGATGCTGAGCTGAGCTTCTTCAATTCGCTCAATACCGAGCTGTATC 360  
Db 301 CAACACTTGCAGATGCTGAGCTGAGCTTCTTCAATTCGCTCAATACCGAGCTGTATC 360  
QY 361 GTCCCGCTCTCTTGTGTAAGGCTGATGATGAAGAAAGTGGAGTGTATACATC 420  
Db 361 GTCCCGCTCTCTTGTGTAAGGCTGATGATGAAGAAAGTGGAGTGTATACATC 420  
QY 421 AATGGCCACTCATCTTCAACCTGTTTGTATCACAACCTGGTGGCGAGCGAGCTC 480  
Db 421 AATGGCCACTCATCTTCAACCTGTTTGTATCACAACCTGGTGGCGAGCGAGCTC 480  
QY 481 CACTCTGTGTGATGAAGGGGTCTCGAAGTGGATGGCAATTCATGTAGAAATTTGGGGC 540  
Db 481 CACTCTGTGTGATGAAGGGGTCTCGAAGTGGATGGCAATTCATGTAGAAATTTGGGGC 540  
QY 541 CAAAACTGGCAAGCAACACTATCTCATGAGGCAAGGCTTCTTCAAGTCACTCTT 600  
Db 541 CAAAACTGGCAAGCAACACTATCTCATGAGGCAAGGCTTCTTCAAGTCACTCTT 600  
QY 601 AGTATGTGTGCACTGCTCATATATCTGTTCTTCAATTTGGCAATTTGGCCAA 660  
Db 601 AGTATGTGTGCACTGCTCATATATCTGTTCTTCAATTTGGCAATTTGGCCAA 660  
QY 661 ACCTATGAAGGCTCTCAATTC 681  
Db 661 ACCTATGAAGGCTCTCAATTC 681

## RESULT 3

US-08-845-539-5

; Sequence 5, Application US/08845539  
; Patent No. 5929303  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Alan B.  
; APPLICANT: Rose, Jocelyn K.C.  
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation  
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/885,970A  
FILING DATE: 19920518  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/617,239  
FILING DATE: 21-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/253,243  
FILING DATE: 04-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 283-2478  
TELEFAX: (608) 251-5139  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 727 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Gossypium hirsutum  
STRAIN: Coker 312  
DEVELOPMENTAL STAGE: 10 day old fiber cells  
TISSUE TYPE: fiber cells  
IMMEDIATE SOURCE:  
LIBRARY: CRFB10  
CLONE: B12  
US-07-885-970A-6

Query Match 38.1%; Score 259.4; DB 1; Length 727;

Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGTCCTCTCCACCAACTTTGGCCCTTAACCTTGTCTCCCTAACAACAATGCT 279  
DB 1 ATACCGTGTACACCAACTTTTGTCCCACTAATGCTTTATCTAGTACATGGC 60  
QY 280 GGATGGTCAACCGCTCTCTCCCAACACTTGCACATGGCTGAGCGCTCTCTTCAATC 339  
DB 61 GGTGTGTGCAATCCCGACAGACACTTGTGATTTGGCGAACCAGCATTTGCGGATA 120  
QY 340 GCTCAATACCGACCTGTATGTCCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399  
DB 121 GCAGAAATATGACCTGGAAATCGTCCCTGTATGTTAGAAAGGTGTCATGTGGAAGAA 180  
QY 400 GGTGAGTGTAGGTTTACATCAATGCGCCTCATTAACCTGCTTTTGTATCACAAC 459  
DB 181 GAGGAGTACAGTACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 460 GTGAGTGGCGCAGGAGCGTCCACTGTGTGATGATGATGATGATGATGATGATGATGAT 519  
DB 241 GTGGGAGGGGCGAGGATTTACAGTGTGTGATGATGATGATGATGATGATGATGATGAT 300  
QY 520 TCCATGTCTAGAAATTTGGGCGCAAAACTGCAAGACAACTATCTCAATGGCCAGGC 579  
DB 301 CCAATGTCCAGAAATTTGGGCGCAAAACTGCAAGACAACTATCTCAATGGCCAGGC 360  
QY 580 CTTTCTTTCAAGTCACTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 639  
DB 361 CTTCTTTTAAAGTCACTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 640 TCCATTTGCAATTTGGCAACCTTGAAGGCGCTCAAT 680

DB 421 GCTGTGTGCAATTCGACCAACTTTTGAAGGAGCGCACTT 461

RESULT 6

US-08-298-687A-6  
Sequence 6, Application US/08298687A  
Patent No. 5521078

GENERAL INFORMATION:

APPLICANT: John, Maliyakal E.

TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON

TITLE OF INVENTION: PLANTS FOR ALTERED FIBER

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nicholas J. Seay, Charles & Brady

STREET: P. O. Box 2113, First Wisconsin Plaza

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/298,687A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,239

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/253,243

FILING DATE: 04-OCT-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 283-2478

TELEFAX: (608) 251-5139

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 727 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Gossypium hirsutum

STRAIN: Coker 312

DEVELOPMENTAL STAGE: 10 day old fiber cells

TISSUE TYPE: fiber cells

IMMEDIATE SOURCE:

LIBRARY: CRFB10

CLONE: B12

US-08-298-687A-6

Query Match 38.1%; Score 259.4; DB 1; Length 727;

Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGTCCTCTCCACCAACTTTGGCCCTTAACCTTGTCTCCCTAACAACAATGCT 279  
DB 1 ATACCGTGTACACCAACTTTTGTCCCACTAATGCTTTATCTAGTACATGGC 60  
QY 280 GGATGGTCAACCGCTCTCTCCCAACACTTGCACATGGCTGAGCGCTCTCTTCAATC 339  
DB 61 GGTGTGTGCAATCCCGACAGACACTTGTGATTTGGCGAACCAGCATTTGCGGATA 120  
QY 340 GCTCAATACCGACCTGTATGTCCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399





FILING DATE: 21-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/253,243  
 FILING DATE: 04-OCT-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27,386  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 283-2478  
 TELEFAX: (608) 251-5139  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 727 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Gossypium hirsutum  
 STRAIN: Coker 312  
 DEVELOPMENTAL STAGE: 10 day old fiber cells  
 TISSUE TYPE: fiber cells  
 IMMEDIATE SOURCE:  
 LIBRARY: CKFB10  
 CLONE: B12  
 US-08-298-829-6

Query Match 38.1%; Score 259.4; DB 1; Length 727;  
 Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
 Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGCTACACCTGTCCTTCCCTTCACTTGTCTCCCTTCAACAACATGCT 279  
 1 ATAAACGTCAGACCACTTTTCCACCTAATGCTTATCTGTGACCAATGCT 60  
 DB 280 GGATGGTACACCTGTCCTTCCACCTGACATGCTGAGGCTCTCTTCAATC 339  
 61 GGGTGGTACATCCCGCAGAGACACTTGTGATTTGGCCGACATCTTGGCGATA 120  
 QY 340 GCTCAATACCGAGCTGATCGTCCCGTCTCCCTTCTGAGGCTACATGATGAAGAA 399  
 121 GCAGAAATATGAGCTGGAATCGTCCCTGTATGTCAGAAAGGTGTCAGTGGAGAA 180  
 DB 400 GTTGAGTACAGTTTCAATCAATGCGCACCTCACTTCAACCTGCTTGTGATCAACAAC 459  
 181 GGAGGATCAGGTACACCAATGATGACATCTGACTTCAACATGCTGTGATGACGAC 240  
 QY 460 GTGAGTGGCAGGACGATCCACTGTCGATGAAGGCTCTGAACTGGATGGCAA 519  
 241 GTGGAGGAGGAGGATATACGTGATGTCATCAAGGTTCCAGAAAGGATGGCTA 300  
 DB 520 TCCATGCTAGAAATTTGGGCGCAAACTGGCAAGCAACATCTATCTGACCAAGC 579  
 301 CCTATGTCAGAAATTTGGGCGCAAACTGGCAAGCAAGTCTTAACTGCGCAAGC 360  
 QY 580 CTTTCCTTAAAGTCTTAACTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 639  
 361 CTCTCTTTAAAGTCTTAACTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 420  
 DB 640 TCCATTTGCAATTTGGCGCAAACTGATGAAGGCTCTCAAT 680  
 421 GCTGGTTGCAATTTGGCGCAAACTTTTGAAGGAGCGCAGTT 461

RESULT 9  
 US-08-787-335-5  
 ; Sequence 5, Application US/08787335  
 ; Patent No. 5981834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John, Maliyakal E.  
 ; APPLICANT: Umbeck, Paul F.

APPLICANT: Brill, Winston J.  
 TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS  
 TITLE OF INVENTION: FOR ALTERED FIBER  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quarles and Brady  
 STREET: P.O. BOX 2113  
 STREET: FIRST WISCONSIN PLAZA  
 CITY: MADISON  
 STATE: WISCONSIN  
 COUNTRY: U.S.A.  
 ZIP: 53701  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh  
 SOFTWARE: Microsoft Word 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/787,335  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/530,797  
 FILING DATE:  
 APPLICATION NUMBER: US 07/253,243  
 FILING DATE: 04-OCT-88  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholas J. Seay  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 1122990245  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 727 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: no  
 ANTI-SENSE: no  
 ORIGINAL SOURCE:  
 ORGANISM: Gossypium hirsutum  
 STRAIN: Coker 312  
 DEVELOPMENTAL STAGE: 10 day old fiber cells  
 TISSUE TYPE: fiber cells  
 IMMEDIATE SOURCE:  
 LIBRARY: CKFB10  
 CLONE: B12  
 US-08-787-335-5

Query Match 38.1%; Score 259.4; DB 2; Length 727;  
 Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
 Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGCTACACCTGTCCTTCCCTTCACTTGTCTCCCTTCAACAACATGCT 279  
 1 ATAAACGTCAGACCACTTTTCCACCTAATGCTTATCTGTGACCAATGCT 60  
 DB 280 GGATGGTACACCTGTCCTTCCACCTGACATGCTGAGGCTCTCTTCAATC 339  
 61 GGGTGGTACATCCCGCAGAGACACTTGTGATTTGGCCGACATCTTGGCGATA 120  
 QY 340 GCTCAATACCGAGCTGATCGTCCCGTCTCCCTTCTGAGGCTACATGATGAAGAA 399  
 121 GCAGAAATATGAGCTGGAATCGTCCCTGTATGTCAGAAAGGTGTCAGTGGAGAA 180  
 DB 400 GTTGAGTACAGTTTCAATCAATGCGCACCTCACTTCAACCTGCTTGTGATCAACAAC 459  
 181 GGAGGATCAGGTACACCAATGATGACATCTGACTTCAACATGCTGTGATGACGAC 240  
 QY 460 GTGAGTGGCAGGACGATCCACTGTCGATGAAGGCTCTGAACTGGATGGCAA 519  
 241 GTGGAGGAGGAGGATATACGTGATGTCATCAAGGTTCCAGAAAGGATGGCTA 300



FILING DATE: 21-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/253,243  
FILING DATE: 04-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 283-2478  
TELEFAX: (608) 251-5139  
INFORMATION FOR SEQ. ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2415 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Gossypium barbadense  
STRAIN: Sea Island  
IMMEDIATE SOURCE:  
LIBRARY: EMBL-SI  
CLONE: SIB12  
US-08-298-687A-26

Query Match 37.2%; Score 253.4; DB 1; Length 2415;  
Best Local Similarity 64.6%; Pred. No. 1.6e-78;

Matches 453; Conservative 0; Mismatches 171; Indels 77; Gaps 2;

57 TGGCACCATTGGTGGAGCTTGTGGATATGGAATTTATACAGCCAGGATATGACGAA 116  
117 CAGGTTGGCCCTGAGACCTGCTATTTAACAATGATTAAGTTGGTGC-TTGCCTCG 175  
1036 CACAGACGCTTGAAGCAGCTGCTTTCAACAATGGCTTGAAGCTGCGTCACTGACG 1095  
176 AATGACTTGTACAGACGACCTAAATGAGTGCCTCCGAGACTATATAGGCTCACTCCA 235  
1096 AGCTCGGTCACATGATGCTCAATGCTGATAGTGAACCATATACCTGACAGCCA 1155  
236 CCACTTTTGGCTCTCACTTGTCTCCCTAACAACAATGATGATGATGACACCTC 295  
1156 CCACTTTTGGCTCTCACTTGTCTCCCTAACAACAATGATGATGATGACACCTC 1215  
296 CTCTCAACACTGACATGCTGAGCTGCTGCTTCAATCCGATACCTGACGCTG 355  
1216 CACGAGACGCTTGAATGCTGAGCTGCTGCTTCAATCCGATACCTGACGCTG 1275  
356 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367  
1276 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1335  
368 -TCTCTTTCGATGAGGTACCATGATGAGGAAA 399  
1336 TTTAAGTATGTTAACTGTTGGGTGTTAACTTTTGGCGTGTGATGTAAGAAA 1395  
400 GGTGAGTATGTTAACTGTTGGGTGTTAACTTTTGGCGTGTGATGTAAGAAA 459  
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460 GTGCGTGGGCGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
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## RESULT 12

US-08-298-829-26  
Sequence 26 Application US/08298829  
Patent No. 5620882  
GENERAL INFORMATION:  
APPLICANT: John, Malyakal E.  
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON  
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nicholas J. Seay, Quarles & Brady  
STREET: P.O. Box 2113, First Wisconsin Plaza  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: USA  
ZIP: 53701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/298,829  
CLASSIFICATION: 800  
FILING DATE: 19-OCT-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/885,970  
FILING DATE: 18-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/617,239  
FILING DATE: 21-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/253,243  
FILING DATE: 04-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 283-2478  
TELEFAX: (608) 251-5139  
INFORMATION FOR SEQ. ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2415 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Gossypium barbadense  
STRAIN: Sea Island  
IMMEDIATE SOURCE:  
LIBRARY: EMBL-SI  
CLONE: SIB12  
US-08-298-829-26

Query Match 37.2%; Score 253.4; DB 1; Length 2415;  
Best Local Similarity 64.6%; Pred. No. 1.6e-78;

Matches 453; Conservative 0; Mismatches 171; Indels 77; Gaps 2;

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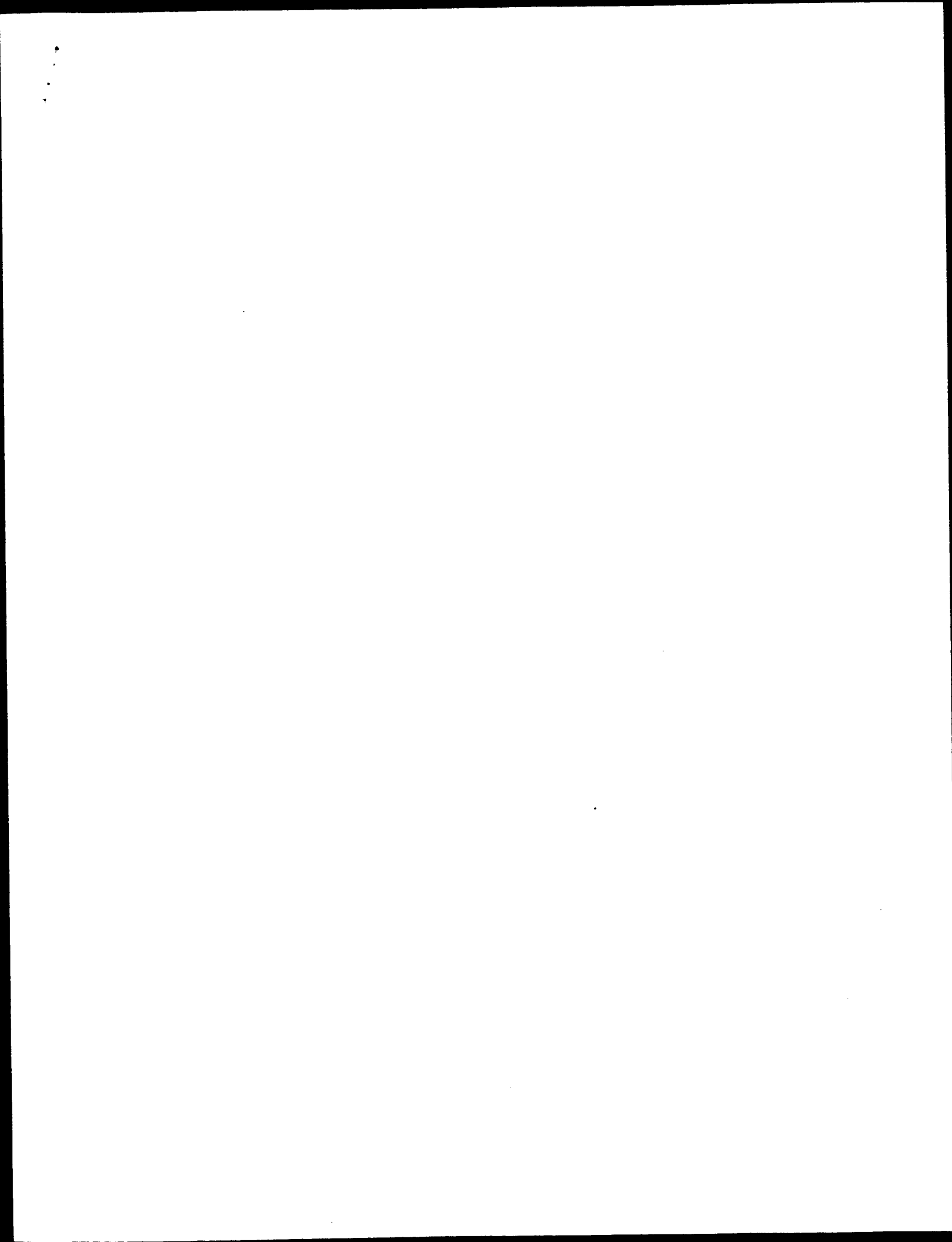
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us-09-896-301-1.rni

Page 11

Search completed: October 13, 2002, 23:35:25  
Job time : 90 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2002, 18:25:39 ; Search time 244 Seconds

(without alignments)  
4791.880 Million cell updates/sec

Title: US-09-896-301-1

Perfect score: 681  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	377.6	55.4	780	21	AAC50628
5	377.6	55.4	1198	21	AAC33521
6	377.6	55.4	1233	21	AAC50633
7	366.6	53.8	1236	21	AAC40035
8	358.6	52.7	1324	21	AAC47530
9	353.8	52.0	1326	21	AAC40169

10	351.4	51.6	1366	21	AAC47991	Arabidopsis thalia
11	350.2	51.4	1212	21	AAC45165	Arabidopsis thalia
12	341.6	50.2	1319	21	AAC44930	Arabidopsis thalia
13	338.2	49.7	1167	22	AA03713	Tomato seed expans
14	338	49.6	1205	21	AAC33121	Arabidopsis thalia
15	331.6	48.7	1201	21	AAC34975	Arabidopsis thalia
16	316.6	46.5	1236	21	AAC34714	Arabidopsis thalia
17	313.6	46.0	488	21	AA293525	Expansin gene sequ
18	313.4	46.0	824	21	AAC24273	Arabidopsis thalia
19	312.8	45.9	1213	22	AA03711	Tomato seed expans
20	301.2	44.2	1037	21	AAC42618	Arabidopsis thalia
21	299.4	44.0	1293	21	AAC37064	Arabidopsis thalia
22	296.2	43.5	1291	21	AAC50400	Arabidopsis thalia
23	287.6	42.2	475	21	AA293526	Expansin gene sequ
24	276.4	40.6	537	20	AAV68448	Melon expansin Cme
25	262.2	38.5	1103	22	AA03712	Tomato seed expans
26	259.4	38.1	727	17	AA730255	Cotton fibre cell-
27	259.4	38.1	727	17	AA73037	Cotton fibre-spect
28	259.4	38.1	727	18	AA70044	Cotton fibre-spect
29	259.4	38.1	727	21	AA762613	Cotton fibre spect
30	259.4	38.1	727	21	AA235549	CDNA sequence a co
31	253.4	37.2	2415	17	AA730268	Cotton fibre clone
32	253.4	37.2	2415	17	AA73053	Cotton fibre-spect
33	253.4	37.2	2415	18	AA70039	Cotton B12 gene an
34	253	37.2	980	21	AAC41263	Arabidopsis thalia
35	250	36.7	702	20	AAV68446	Tomato expansin Le
36	242.8	35.7	448	21	AA293530	Expansin gene sequ
37	242.8	35.7	501	20	AAV68447	Strawberry expans
38	222.2	32.6	1132	21	AAC38981	Arabidopsis thalia
39	218.2	32.0	695	21	AAC41531	Arabidopsis thalia
40	208.8	30.7	1141	21	AAC33606	Expansin gene sequ
41	204.6	30.0	437	21	AA293528	Expansin gene sequ
42	204.6	30.0	437	21	AA293529	Expansin gene sequ
43	177	26.0	1137	21	AAC47343	Arabidopsis thalia
44	177	26.0	1143	21	AAC38217	Arabidopsis thalia
45	163.2	24.0	494	21	AA293527	Expansin gene sequ

#### ALIGNMENTS

RESULT 1	
AAAT13320	AAAT13320 standard; DNA; 681 BP.
AC	AAAT13320;
AC	08-JUL-1996 (first entry)
DT	Cucumis sativus var. Burpee Pickler.
XX	Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
XX	polysaccharide; cucumber; ss.
XX	Cucumis sativus var. Burpee Pickler.
OS	AU9540262-A.
XX	04-APR-1996.
PD	12-MAY-1994; 94AU-0068320.
XX	12-MAY-1995; 95US-0440517.
XX	12-MAY-1993; 93US-0060944.
PR	(PENN-) PENN STATE RES FOUND.
XX	Cosgrove DJ, McQueen-Mason S;
XX	WPI. 1996-201150/21.
DR	P-PSDB; AAR94527.
XX	Expansin proteins which alter the mechanical strength of

PT poly:saccharide(s) - useful in paper mfr. and recycling  
XX  
PS Disclosure; Page 30; 60pp; English.

xxv Disclosure; Page 30; 60pp; English.

CC A cDNA clone (AA113320) codes for cucumber expansin-29 (AA094527),  
CC a member of a novel class of proteins that catalyse the extension of  
CC plant cell walls and the weakening of the hydrogen bonds in pure  
CC cellulose. It was obtd. by PCR amplification of cucumber seedling  
CC cDNA using primers based on isolated peptide fragments of the protein.  
CC The gene can be expressed in bacterial or other systems for use in  
CC recombinant expansin prodn. Expression of the gene in transgenic  
CC plants may allow alteration of plant growth characteristics.  
CC While expression in plant tissue cultures may allow improved prodn.  
CC of useful chemicals.

50 Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;

Query Match	100.08;	Score 681;	DB 17;	Length 681;
Best Local Similarity	100.08	Prod No 1	88-338	

Best Local Similarity 100.0%; Pred. No. 1.8e-228,  
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Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GACTACGGTGGCTGGCAGAGCGGCCACCTTTATGGTGGTGACGCATCTGC 60

61 ACCATGGGTGAGCTTGTGGTATGGAAATTATACAGCCAAGGTATGGCAGAACACG 120

Db 61 ACCATGGGTGAGCTTGTGGGTATGGAAATTATACAGCCAGGGTATGGCAGACACG 120

121 GTGGCGCTGAGCACTGGCGTATTTAACAATGGATTAGTTGTGGTCTTGCTTCGAATG 180

Db 121 GTGGCGCTGAGCACTGCGCTATTTAACAATGGATTAGTTGTGGTGCCTTGCTCGAATG 180

181 ACTTGTAACAACGACCCTAATGGTGCTTCGGGAAGTATAGGGTCACTGCCACCAAC 240

Db 181 ACTTGTAACAACGACCCTAAATGGTGCTTCGGGAACTATTAGGCTCACTGCCACCAAC 240

241 TTTTGCCCTCCTAAGTTGGCTCTCCCTAACACACAAATGGTGATGGTGCAACCTCCTCTC 300

Db 241 TTTGGCCCTCCTAACTTTGCTCTCCCTAACACACAA<sup>T</sup>GGTGATGGTGCAACCTCCTC 300

301 CAACACTTCGACATGGCTGAGCCTGCCCTTCCTTCAATCGCTCAATACCGAGCTGGTATC 360

Db 301 CAACACTTCGACATGGCTGAGCCCTGCCCTTCCTTCAATCGCTCAATACCGAGCTGGTATC 360

361 GTCCCCGTCCTTCGTAGGGTACCATGTATGAAGAAAGCTGGAGTGAGTTACAATC 420

Db 361 GTCCTCTCCCTTTCGTAGGGTACCATGTATGAAGAAAGGTGGAGTGAGGTTACAATC 420

421 AATGCCACTCATCTCAACCTCGTTTGATCACAAACGTCGGTGGCCGACGCACGTC 480

Db 421 AATGGCACTCATACTCAACCTCGTTTGATCACAAACGTGGGCGAGGGGACGTC 480

481 CACTCTGTTCGATAAGGGCTCTCGAACTGGATGGCAATCCATGCTAGAAATGGGC 540

Db 481 CACTCTGTGTCGATAAAGGGGTCTCGAACTGGATGGCAATCCATGCTCTAGAAATTGGGC 540

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DB 541 CAAACCTGGCAAGCAACACTATCTCAATGGCCAAGGCCTTTCCTTCAAGTCACTCTT 600

QY 601 AGTGAATGGTCGCACCTCTCACTGCGCTATAATCTCGTTCCTTCCAATTGGCAATTGGCCAA 660

601 AGTGAATGGTGGCACTCTCCTATATCTCGTTCCCTTCCAATTGGCCAA 660

661 ACCCTATGAAGGCCCTCAATTTC 681

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## RESULT 2

AAC48712

IP AAC48712 standard; DNA; 1015 BP.

Tue Oct 15 18:05:20 2002

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ID AAC50628 standard; DNA: 780 BP.  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
PN EP1033405-A2.  
XX  
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QY	482	ACTCTGTTCGATTAAGGGGCTCTGGAACCTGGATGGCAATCATATGTCTAAGAAATTTGGGGCC	541
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KW Hybridisation assay; genetic mapping; gene expression control;  
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DB 291 GGGAGAGCTTGTGGTATGGAATTTATACAGCAAGGATGGCAGCAACACGCGTGC 350
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Db 651 CAAGCGTACCGTTACTTCAACTTGTCTGTATCATCTAGCTGCTGAGCAGAGCAT 710
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QY 540 CCAAACTGGCAAAAGCAGCACTATCTCATATGGCCAAAGCCTTTCCTTCAACTGACT 599
Db 771 ACAAACCTGGCAATCTTAATGCTGTTGTGTGTGATGATGCACTCTTCCCTGTCAAG 830
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Db 831 CAGTACCGGTAGAACATCTACTTCTGTGAACATGTGTTCTTCACTGCGAGTTGGTCA 890
QY 660 AACCTAGAGGCCCTCTCAATTG 681
Db 891 AACCTTGTGCGAAGAAATTTG 912

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## RESULT 13

AD03713 standard; cDNA; 1167 BP.

AD03713:

19-JUN-2001 (first entry)

Tomato seed expansin, *LeEXP10*, cDNA for controlling seed germination.

Tomato: endo-beta-mannanase; Lycopersicon esculentum mannanase2; LEMAN2;  
 polygluturonase; PG; *LeEXP1*; cellulase; arabinosidase; *LeEXP*;  
 xyloglucan endotransglycosylase; XET; *LeEXP4*; expansin; *LeEXP8*;  
*LeEXP10*; hydrolase; endosperm cap; tissue weakening; radicle growth;  
 seed germination; ss.

Lycopersicon esculentum.

key Location/Qualifiers  
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W0200123530-A1.

05-APR-2001.

29-SEP-2000; 2000MO-US26884.

30-SEP-1999; 99US-0410191.

(REGC ) UNIV CALIFORNIA.

Bradford KJ, Chen F, Dahal P, Downie B, Nonogaki H;



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PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151348.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156586.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.

Query Match	Similarity	48.7%	Score 331.6	DB 21	Length 1201
Best Local	Similarity	48.2%	Pred. 0.14e-105		
Matches	460	Conservative	0	Mismatches 214	Indels 0
				Gaps	0
QY	8	GTGGCTGGCAGAGCGGCCAGCCACCTTTTATGTTGGTGGTACGCATCTGGCACCATGG	67		
DB	184	GTGGTTGGGTCAATGCTCCAGCCACATCTTATGAGAGACCTGATGCTTCCGACACATGG	243		
QY	68	GTGGAGCTTGTGGGTATGGGAATTATACGGCAAGGATATGGCAAGACAGGTGGCC	127		
DB	244	GGGGGGCGGTGGTTACGGAAACTTATACGTCAAGGATAGGSCATTAACAGCGGGCTC	303		
QY	128	TGAGCACTGGCTATTATTAACAATGGATTAAAGTTGGTGGCTTTGCTTCAAAAGACTTGT	187		
DB	304	TAAAGCAGCGCTCTATTATTCACAGCGGGCCAAAGCTGTGGTCTTGTTTCAAGTAAATGG	363		
QY	188	CAAGAGACCCCTAAATGTGTGCTTCGGGGAACTATTAGGTCACTGCACCAACTTTGCC	247		
DB	364	TGAGCAGCCCAAAATGTGTATCGGTGAAACATCAACCTCAACGGAAACAACTTTTGTC	423		
QY	248	CTCTCACTTGTCTCTCTCCCTAACAAATAGTGGATGTGCAACCCCTCTCTCAACACT	307		
DB	424	CACCCAACTTGTCTCAAGSCAACACAGCCGGAGTGGTGTATCTCTTCAACACACT	483		
QY	308	TGACATAGGCTGAGCGCTGCTTCTTCAATCGCTCAATACGAGCTGTAATGTCGCCG	367		
DB	484	TGGAATTTACTCAGGCCATCTTCCCGTATTTGCTCAATAAGAGCGGCGCTGTCGCCG	543		
QY	368	TCTCCCTTGTGGGAGACCATGATGAAGAAAGGTGGATGTGAGTTATCAATCAATGGCC	427		
DB	544	TCCATTAACGGAGATGGCTTCCCGGAGAAAAGAGAAATTAAGATTCAAGATCAACGGTC	603		
QY	428	ACTCATCTTCAACCTCGTTTTGATCACAAACGTGGGTGGCGCAGGCGAGCTCACTG	487		
DB	604	ATTCTACTTCAACCTCGTATTTATTAACCAAGCTGGCGCGCCGGAATGTTATCTCGG	663		
QY	488	TGTGATTAAGGGGTCTGCAACTGGATGGCAATCCATGTCTTGAATTTGGGGCCAAACT	547		
DB	664	TCTCATTTAAAGAAACCAATACACGTGTGGCAAGCATGTCAAGAAATCTGGGAGCAGAAT	723		
QY	548	GGCAAGCAACAACTATCTCAATGGCAGAGGCTTTCTCTTCAAGTCACTTATAGTATG	607		
DB	724	GGCAAGCAATCAAAACTGTGATGGTCAAGCTTTGTCTTTAAAGTAACTAAGTATGATG	783		
QY	608	GTGCACTCTCACTGCTTATTAATCTGTTCTTCCAATTGGGCAATTTGGCAACCTATG	667		
DB	784	GGCTTACAGATTATTACTAACAATGCTACACAGTAACTGAGGCTTGGAGCAAGCTATTA	843		

Oy 668 AAGCCCTCAATTC 681  
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Db 844 CCGGAAACAGTTC 857

Search completed: October 13, 2002, 23:03:27  
Job time : 251 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2002, 18:25:39 : Search time 1809 Seconds

(without alignments)  
7877.817 Million cell updates/sec

Title: US-09-896-301-1

Perfect score: 681  
Sequence: 1 gactacgctgctgcgcagag.....cctatgaagccctcaattc 681

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
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5: gb\_ov:\*  
6: gb\_pat:\*  
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12: gb\_sy:\*  
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30: em\_hlg\_hum:\*  
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32: em\_hlg\_other:\*  
33: em\_hlg\_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Length	DB	ID	Description
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1	681	100.0	681	6	AR076514
2	681	100.0	681	6	AR161478
3	681	100.0	684	6	AX306490
4	681	100.0	992	6	CSU30382
5	676.2	99.3	681	6	AX306492
6	438.4	64.4	1109	8	PAU93167
7	433.6	63.7	1035	8	CAR291817
8	433.6	63.7	1177	8	AF049354
9	427.2	62.7	1048	8	AF297521
10	427.2	62.7	1109	8	AF350937
11	420.6	61.8	1233	8	AF350936
12	417.6	61.3	1180	8	AF159563
13	414.4	60.9	1147	8	AF0967176
14	409.6	60.1	1088	8	AF230332
15	409.4	60.1	1220	8	AB029083
16	407.8	59.9	1252	8	AF038815
17	401.4	58.9	1173	8	AF167360
18	383.8	56.4	1419	8	AF448467
19	383.6	56.3	1219	8	OS085246
20	380.8	55.9	1102	8	AF043284
21	380.6	55.9	1172	8	AF350938
22	380.6	55.9	1339	8	AF297522
23	378.8	55.8	1323	8	OSU30477
24	378.8	55.6	891	8	PTU64893
25	377.6	55.4	750	8	AV060512
26	377.6	55.4	1189	8	AF229437
27	377.6	55.4	1238	8	AV052247
28	374	54.9	919	8	PTU64891
29	374	54.9	998	8	AF085330
30	372.2	54.7	1090	8	AF332169
31	370.8	54.4	923	8	PTU64890
32	367.6	54.0	923	8	PTU64892
33	363	53.3	926	8	ATU30481
34	361.4	53.1	687	6	AX306496
35	360.6	53.0	749	8	ATU30476
36	360.6	53.0	784	8	ATU30477
37	360.6	53.0	1339	8	AF360291
38	359.8	52.8	994	8	AV064035
39	358.6	52.7	1384	8	AV072167
40	358.2	52.6	1389	8	AF049353
41	346.6	50.9	1263	8	AF230276
42	345.2	50.7	660	8	AB049406
43	342.2	50.2	545	8	GMA289154
44	341.6	50.2	1306	8	AF410277
45	341.6	50.2	1318	8	AV062683

## ALIGNMENTS

RESULT 1  
LOCUS AR076514 681 bp DNA linear PAT 30-AUG-2000  
DEFINITION Sequence 1 from patent US 5959082.  
ACCESSION AR076514  
VERSION AR076514.1 GI:10003260  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 681)  
AUTHORS Cosgrove,D.J., McQueen-Mason,S., Gullinan,M., Shcherban,T. and Shi,J.

TITLE Proteins catalyzing the extension of plant cell walls  
JOURNAL Patent: US 5959082-A 1 28-SEP-1999;  
FEATURES Location/Qualifiers  
source  
1..681  
/organism="unknown"

BASE COUNT 161 a 179 c 164 g 177 t  
Query Match 100.0%; Score 681; DB 6; Length 681;  
Best Local Similarity 100.0%; Pred. No. 9e-199;

Matches 681: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACTACGGTGGCTGGCAGAGCGGCGACGCCCTTTATGGTGGTGGTGGCATTGGC 60  
 Db 1 GACTACGGTGGCTGGCAGAGCGGCGACGCCCTTTATGGTGGTGGTGGCATTGGC 60  
 Oy 61 ACCATGGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATATGGCAGACAG 120  
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 Oy 121 GTGGCGCTGAGCACTGGCTATTTAACAATGATTAAGTGTGGTGGTGGTGGTGAATG 180  
 Db 121 GTGGCGCTGAGCACTGGCTATTTAACAATGATTAAGTGTGGTGGTGGTGGTGAATG 180  
 Oy 181 ACTGTACAAAGCAGCCCTAAATGGTGGCTTCCGGGAACCTATTAGGTCACAGCCAC 240  
 Db 181 ACTGTACAAAGCAGCCCTAAATGGTGGCTTCCGGGAACCTATTAGGTCACAGCCAC 240  
 Oy 241 TTTTGCCCTGCTACCTTGTCTCTCCCTAACAAACAAATGGTGGTGGTGGTGGTGGT 300  
 Db 241 TTTTGCCCTGCTACCTTGTCTCTCCCTAACAAACAAATGGTGGTGGTGGTGGTGGT 300  
 Oy 301 CAACACTTGCAGATGGCTGAGCGCTGCTCTTCAATCGCTCAATACGAGCTGGTATC 360  
 Db 301 CAACACTTGCAGATGGCTGAGCGCTGCTCTTCAATCGCTCAATACGAGCTGGTATC 360  
 Oy 361 GTCCCGCTGCTCTTGTAGAGGTACATGTATGAAGAAGGTGGATGGAGTGTACATC 420  
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 Db 481 CACTCTGTGTGATTAAGGGGTCTCGAAGTGGATGGCAATCGATGTAGAAATTTGGGG 540  
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 Db 541 CAAACCTGGCAAGCAACACTATCTCAATGGCCAAAGGCTTCTTCAAGTCACTCTT 600  
 Oy 601 AGTATGTGTGCACTCTGCTATATCTGCTTCTTCCCAATTTGGCCAA 660  
 Db 601 AGTATGTGTGCACTCTGCTATATCTGCTTCTTCCCAATTTGGCCAA 660  
 Oy 661 ACCATGAGAGGCGCTCAATTC 681  
 Db 661 ACCATGAGAGGCGCTCAATTC 681

RESULT 2  
 ARI61478 681 bp DNA linear PAT 17-OCT-2001  
 LOCUS Sequence 1 from patent US 6255466.  
 DEFINITION ARI61478  
 ACCESSION ARI61478  
 VERSION ARI61478.1 GI:16227385  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 681)  
 AUTHORS Cosgrove,D.J., McQueen-Mason,S., Gullinan,M., Shcherban,T. and Shl,J.  
 TITLE Purified plant expansion proteins and DNA encoding same  
 JOURNAL Patent: US 6255466-A 1 03-JUL-2001.  
 FEATURES Location/Qualifiers  
 source 1..681

BASE COUNT 161 a 179 c 164 g 177 t  
 ORIGIN  
 Query Match 100.0%; Score 681; DB 6; Length 681;

Best Local Similarity 100.0%; Pred. No. 9e-199;  
 Matches 681: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACTACGGTGGCTGGCAGAGCGGCGACGCCCTTTATGGTGGTGGTGGCATTGGC 60  
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 Db 61 ACCATGGGTGGAGCTTGGGTATGGGAATTTATACAGCCAAAGGATATGGCAGACAG 120  
 Oy 121 GTGGCGCTGAGCACTGGCTATTTAACAATGATTAAGTGTGGTGGTGGTGGTGAATG 180  
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 Oy 241 TTTTGCCCTGCTACCTTGTCTCTCCCTAACAAACAAATGGTGGTGGTGGTGGTGGT 300  
 Db 241 TTTTGCCCTGCTACCTTGTCTCTCCCTAACAAACAAATGGTGGTGGTGGTGGTGGT 300  
 Oy 301 CAACACTTGCAGATGGCTGAGCGCTGCTCTTCAATCGCTCAATACGAGCTGGTATC 360  
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 Db 361 GTCCCGCTGCTCTTGTAGAGGTACATGTATGAAGAAGGTGGATGGAGTGTACATC 420  
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 Db 541 CAAACCTGGCAAGCAACACTATCTCAATGGCCAAAGGCTTCTTCAAGTCACTCTT 600  
 Oy 601 AGTATGTGTGCACTCTGCTATATCTGCTTCTTCCCAATTTGGCCAA 660  
 Db 601 AGTATGTGTGCACTCTGCTATATCTGCTTCTTCCCAATTTGGCCAA 660  
 Oy 661 ACCATGAGAGGCGCTCAATTC 681  
 Db 661 ACCATGAGAGGCGCTCAATTC 681

RESULT 3  
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 LOCUS Sequence 1 from Patent WO0188163.  
 DEFINITION AX306490  
 ACCESSION AX306490  
 VERSION AX306490.1 GI:17645710  
 KEYWORDS  
 SOURCE Cucurbit.  
 ORGANISM Cucumis sativus

REFERENCE 1 (sites)  
 AUTHORS Berendes,F., Rast,H.G., Vogt,U. and Gouloudis,C.  
 TITLE Method for producing recombinant expansins  
 JOURNAL Patent: WO 0188163-A 1 22-NOV-2001;  
 Bayer Aktiengesellschaft (DE)  
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BASE COUNT 163 a 179 c 164 g 178 t

ORIGIN

Query Match 100.0%; Score 681; DB 6; Length 684;  
Best Local Similarity 100.0%; Pred. No. 9e-199;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 GTGGCGGTGACGACGTGGCTATTTAACAATGATTAAGTTGTGCTTGTGCAATG 180  
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181 ACTTGTACAAAGACCCCTAATGATGTCGCGGAATTAAGGTCACCTGCGACCAAC 240  
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241 TTTTGGCCCTCTAATCTTGTCTCCCTACCAACAATGTGGATGGTGAACCCCTCTC 300  
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361 GTCCCGCTCTCTTGTGTAGGATGATGATGATGATGATGATGATGATGATGATG 420  
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421 AATGGCCACATCACTTCAACGCTGTTTGTATCAACAAGCTGGTGGCGAGCGATC 480  
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661 ACCTATGAAGGCCCTCAATTC 681  
661 ACCTATGAAGGCCCTCAATTC 681

RESULT 4  
CSU30382 992 bp mRNA linear PLN 04-DEC-1996  
LOCUS Cucumis sativus expansin (Cs-Exp1) mRNA, complete cds.  
DEFINITION  
ACCESSION U30382  
VERSION U30382.1 GI:1040874  
KEYWORDS

SOURCE

ORGANISM cucurbit.  
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
Rosidae: eustosids I: Cucurbitales: Cucurbitaceae: Cucumns.  
1 (bases 1 to 992)  
2 (bases 1 to 992)  
AUTHORS Sheehar, T.Y., Shi, J., Duracko, D.M., Gullitman, M.J.,  
McQueen-Mason, S.J., Sheehar, M. and Cosgrove, D.J.  
TITLE Molecular cloning and sequence analysis of expansins--a highly  
conserved, multigene family of proteins that mediate cell wall  
extension in plants  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)  
MEDLINE 96016146  
REFERENCE 2 (bases 1 to 992)  
AUTHORS Sheehar, T.Y., Shi, J., Duracko, D.M., Gullitman, M.J.,  
McQueen-Mason, S.J., Sheehar, M. and Cosgrove, D.J.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania  
State University, 208 Mueller Laboratory, University Park, PA  
16802, USA

FEATURES

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polyA\_site  
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ORIGIN

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223 GACTACGGTGGCTGCGAGACGGCCACGCTTTTATGTGGTGGTACGACATCTGC 282  
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121 GTGGCGGTGACGACGTGGCTATTTAACAATGATTAAGTTGTGCTTGTGCAATG 180  
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403 ACTTGTACAAAGACCCCTAATGATGTCGCGGAATTAAGGTCACCTGCGACCAAC 462  
241 TTTTGGCCCTCTAATCTTGTCTCCCTACCAACAATGTGGATGGTGAACCCCTCTC 300  
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QY	301	CAACACTTCGACATATGGCTGAGCCTGCGCTTCCTTCAAAATGCTCATAATACGAGCTGATAC	360
Db	523	CAACACTTCGACATATGGCTGAGCCTGCGCTTCCTTCAAAATGCTCATAATACGAGCTGATAC	582
QY	361	GTCCCGCTGCTCCTTTCGTATGGGCTTACCATGTATGAAGAAGGTGGAGTGAAGTTTACAAAC	420
Db	583	GTCCCGCTGCTCCTTTCGTATGGGCTTACCATGTATGAAGAAGGTGGAGTGAAGTTTACAAAC	642
QY	421	AATGGCCACTCACTACTTCAACCTGCTTTTGATACAAACGTCGGTGGCGCAGCGCAGCTC	480
Db	643	AATGGCCACTCACTACTTCAACCTGCTTTTGATACAAACGTCGGTGGCGCAGCGCAGCTC	702
QY	481	CACCTGTGTGATATAAGGGGTCTCGAAGCTGGATGGCAATCCATGTCTTGAATAATTTGGGCG	540
Db	703	CACCTGTGTGATATAAGGGGTCTCGAAGCTGGATGGCAATCCATGTCTTGAATAATTTGGGCG	762
QY	541	CAAAACTGGCAAGCAACAACTATCTCAATGCGCCAAAGGCTTTCCTTCAAGTCACTCTT	600
Db	763	CAAAACTGGCAAGCAACAACTATCTCAATGCGCCAAAGGCTTTCCTTCAAGTCACTCTT	822
QY	601	AGTGAATGCTGCACCTCTCACTGCTATATACTCGTTCTTCCCAATTTGGCAATTTGGCCAA	660
Db	823	AGTGAATGCTGCACCTCTCACTGCTATATACTCGTTCTTCCCAATTTGGCAATTTGGCCAA	882
QY	661	ACCTATGAAGGCCCTCAATTC 681	
Db	883	ACCTATGAAGGCCCTCAATTC 903	

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AX306492	LOCUS	AX306492	
DEFINITION	Sequence	3 from Patent WO0188163.	DNA linear PAT 11-DEC-2001
ACCESSION	AX306492		
VERSION	AX306492.1	GI:17645712	

REFERENCE  
1 (sites)  
Berendes, F., Rast, H.G., Vogt, U. and Gouloudis, C.  
Method for producing recombinant expansins  
Patent: WO 0188163-A 3 22-NOV-2001;

FEATURES	Location/Qualifiers
source	1. .681

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Query Match	99.3%	Score 676.2	DB 6	Length 681
Best Local Similarity	99.6%	Pred. No. 2,7e-197		
Matches 678; Conservative	0	Mismatches 3	Indels 0	Gaps 0

Qy 1 GACTACGGTGGCTGGCAGAGCGGGCCAGCCACTTTATGGTGGTGGTACCATCTGGC 60  
Db 1 GACTACGGTGGCTGGCAGAGCGGGCCAGCCACTTTATGGTGGTGGTACCATCTGGC 60

QY	61	ACATATGGGTGGAGCTCTTGTGGGTATGTGGAAATTTATACACCCAAAGGATATGGACACGAACACG	120
Db	61	ACCAATGGGTGGAGCTGTGTGGGTATGTGGAAATTTATACACCCAAAGGATATGGACACGAACACG	120
QY	121	GTGGGCGTGAGACACTGACCCTATTTTAAACAATGGATTAAAGTTGTGGGCTTGGCTTGCAGATG	180
Db	121	GTGGGCGTGAGACACTGACCCTATTTTAAACAATGGATTAAAGTTGTGGGCTTGGCTTGCAGATG	180
QY	181	ACTTGTACAAAGACACCTTAATGTGCTTCCGGGACTATTATAGGGTCATGCGCACCAAC	240
Db	181	ACTTGTACAAAGACACCTTAATGTGCTTCCGGGACTATTATAGGGTCATGCGCACCAAC	240
QY	241	TTTTCCCTCCCTAAATTTGTCTCTCCCTAAACAACAATGGTGATGGGTGGGTGCACCCCTCCTC	300
Db	241	TTTTCCCTCCCTAAATTTGTCTCTCCCTAAACAACAATGGTGATGGGTGGGTGCACCCCTCCTC	300
QY	301	CAACACTTGCACATGGCTGAGAGCTGCGCTTCCTTCAAAATCGCTCAATACCGAGCTGATATC	360
Db	301	CAACACTTGCACATGGCTGAGAGCTGCGCTTCCTTCAAAATCGCTCAATACCGAGCTGATATC	360
QY	361	GTCCCCGCTCCTCTTGTGAGGGTACCCATGTATGAAAGAAAGTGGACATGAGCTTATCAATC	420
Db	361	GTCCCCGCTCCTCTTGTGAGGGTACCCATGTATGAAAGAAAGTGGACATGAGCTTATCAATC	420
QY	421	AATGGCCACTCATACTTAACTTAACCTCGTTTTGATTCACAACAGCTCGGTGGGCGACGAGAGTC	480
Db	421	AATGGCCACTCATACTTAACTTAACCTCGTTTTGATTCACAACAGCTCGGTGGGCGACGAGAGTC	480
QY	481	CACCTGTGTGTGATTAAGAGGGGTCTGCAACTGGAATGGCCATTCATATGTCTAGAAATTTGGGGC	540
Db	481	CACCTGTGTGTGATTAAGAGGGGTCTGCAACTGGAATGGCCATTCATATGTCTAGAAATTTGGGGC	540
QY	541	CAAAACTGGCAAGCAACAACTATCTCAATGAGCCAAAGGCCCTTTCCTTCAAGTCACATCTT	600
Db	541	CAAAACTGGCAAGCAACAACTATCTCAATGAGCCAAAGGCCCTTTCCTTCAAGTCACATCTT	600
QY	601	AGTGTGTGTGCTACTCTCTACTGTCTATATATCTGTTTCCCTTCCAAATTTGGCCAA	660
Db	601	AGTGTGTGTGCTACTCTCTACTGTCTATATCTGTTTCCCTTCCAAATTTGGCCAA	660
QY	661	ACCTATGAAAGGCCCTCAATTC	681
Db	661	ACCTATGAAAGGCCCTCAATTC	681

LOCUS	PAU093167	1109 bp	mRNA	linear	PLN 01-SEP-1998
DEFINITION	Pernus artemisiaca expansin (Pa-Exp1) mRNA, complete cds.				
ACCESSION	U93167				
KEYWORDS	U93167.1	GI:3510537			
SOURCE	apricot.				

REFERENCE  
1 (bases 1 to 1109)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

**AUTHORS** Mbeugue-A-Mbeugue, D., Gomez, R.-M., and Fils-Lycao, B.  
**TITLE** Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1) from apricot fruit  
**JOURNAL** unpublished

REFERENCE  
2 (bases 1 to 1109)  
AUTHORS  
Meguie-A-Meguie,D., Gomez,R.-M. and Fils-Lycaon,B.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (12-MAR-1997) Station de Technologie des Produits

TITLE	Direct Submission
JOURNAL	Submitted (12-DEC-1997) Station de Technologie des Produits Vegetaux, INRA, Site AGROPARC, Avignon 84914 Cedex 9, France
REMARK	Sequence update by submitter

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source  
Location/Qualifiers  
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BASE COUNT 301 a 254 c 242 g 312 t

ORIGIN  
Query Match 64.4%; Score 438.4; DB 8; Length 1109;  
Best Local Similarity 77.8%; Pred. No. 6.2e-124;  
Matches 529; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 1 GACTACGCTGGCTGGCAGACGGCCAGCCACCTTTATGCTGTGACGATCTGGC 60  
DB 155 GATTATGCTGGCTGGAGGCGCTCATGCCCTTTTATGTGGCGGTGATGGCTGGGA 214  
QY 61 ACCATGGGTGGAGCTTGGGTATGGAAATTTATACAGCAAGGATGGCAGCAACAG 120  
DB 215 ACCATGGGGGAGCATGTGGTATGGAACTTTGACAGCAAGGATGGAAACCACT 274  
QY 121 GTGGCGTGAAGCTGGCTTTTACCAATGATTAAGTTGGTGGCTTCTCGAATG 180  
DB 275 GCAGCTTTAAGACAGCCCTTTTAAACATGGCTTGAGCTGGCTTTGTATGAATG 334  
QY 181 ACTGTACAAAGACGCTTAATGGTCCGGGAACTATTAGGCTACTGCCAAC 240  
DB 335 ACATGCAACAATGACCTTATGATGTGCTGTGGAACATCATTTACTGCCAACAC 394  
QY 241 TTTTGCCCTCTAATCTTCTCTCCCTTAACAACAATGGTGAATGCCACCTCTC 300  
DB 395 TTTTGCCCTCTAATCTTCTCTCCCTTAACAACAATGGTGAATGCCACCTCTC 454  
QY 301 GAACACTGGACATGGCTGAGCTGCTTCTTCAAAATGGCTCAATACCAAGCTGTATC 360  
DB 455 CAGCACTTTGATTTGGCTGAGCTGCTTCTTCAAAATGGCCAAATACCGCGTGGAT 514  
QY 361 GTCCCGCTCTCTTCTGATGGTACCATGTATGAAGAAAGTGGAGTGAATTAACATC 420  
DB 515 GTGCTGTACTCTTCAAGAGAGTGGCTGTATGAAGAAAGGAGATAGATCAATC 574  
QY 421 AATGGCCACTCATCTTCAACCGCTTTTATCAAAAGTGGGCGGAGGAGCTC 480  
DB 575 AATGGCCACTCATCTTCAACCGCTTTTATCAAAAGTGGGCGGAGGAGCTC 634  
QY 481 CACTGTGTGATTAAGGGGCTCGAACTGGATGGCAATCATGTATGAATTTGGGGC 540  
DB 635 CACTGTGTGATTAAGGGGCTCGAACTGGATGGCAATCATGTATGAATTTGGGGC 694  
QY 541 CAAACTGGCAAGCAACATCTATCGCAAGGCGCTTCTTCAAGTCACTCTT 600  
DB 695 CAAAACTGGCAAGCAACATCTATCGCAAGGCGCTTCTTCAAGTCACTCTT 754  
QY 601 AGTATGTGCTGCTCACTGCTTATATCTGTTCTTCAATTTGGCAATTTGGCCAA 660  
DB 755 AGTATGTGCTGCTCACTGCTTATATCTGTTCTTCAATTTGGCAATTTGGCCAA 814  
QY 661 ACCTATGAAGGCTCTCAATT 680

DB 815 ACTTCTCAGGGGCTCAATT 834  
RESULT 7  
CAR291817 1035 bp mRNA linear PLN 19-DEC-2000  
LOCUS Cicer arietinum mRNA for expansin, clone CanExp-2.  
DEFINITION AJ291817  
ACCESSION AJ291817.1 GI:11932091  
VERSION  
KEYWORDS expansin.  
SOURCE chickpea.  
ORGANISM Cicer arietinum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae;  
Cicer.  
1 (bases 1 to 1035)  
Doplico, B., Sanchez, M.A. and Labrador, E.  
An second expansin is expressed in chickpea epicotyls  
unpublished  
2 (bases 1 to 1035)  
Labrador, E.  
Direct Submission  
Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal,  
Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la  
Reina s/n, E-37007, SPAIN  
Location/Qualifiers  
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BASE COUNT 312 a 168 c 213 g 342 t

ORIGIN  
Query Match 63.7%; Score 433.6; DB 8; Length 1035;  
Best Local Similarity 77.4%; Pred. No. 1.9e-122;  
Matches 526; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 1 GACTACGCTGGCTGGCAGACGGCCAGCCACCTTTATGCTGTGACGATCTGGC 60  
DB 129 GATTATGCTGGCTGGAGGCGCTCATGCCCTTTTATGTGGCGGTGATGGCTGGGA 188  
QY 61 ACCATGGGTGGAGCTTGGGTATGGAAATTTATACAGCAAGGATGGCAGCAACAG 120  
DB 189 ACAATGGGTGGAGCATGTGATATGTAATTTGTAAGCAAGATATGGAACCAACCA 248  
QY 121 GTGGCGTGAAGCTGGCTGATTTAACAATGATTAAGTTGGTGGCTTCTCGAATG 180  
DB 249 GCAGCACTAAGCACTGCTTATTAACAATGTTTAAGTTGGATCTTGTATGAATG 308  
QY 181 ACTGTACAAAGCAACCTTAATGTCCTTCCGGAACATTAAGGTCACATGGCCACAC 240  
DB 309 AGATGAATGATGATCCAGATGTGTCAAACTGGCTCTTATTTGTTATGTCACAAAT 368  
QY 241 TTTTGCCCTCTAATCTTGGCTCTCCCTTAACAACAATGATGGATGGCAACCTCTCTC 300  
DB 369 TTTTGCTCACCAATTCATCTTTGGCTAATTAATGATGGTGGTGAACCTCTCTTG 428

Query Match	63.7%	Score 433.6	DB 8	Length 1177
Best Local Similarity	77.4%	Pred. No. 1.9e-122		
Matches 526	Conservative 0	Mismatches 154	Indels 0	Gaps 0
QY 1	GACTACGCTGGCTGGCAGAGCGGCCACGGCACCTTTATAGTGTGTGTGAGCATCTGGC 60			
Db 67	GATTATGCTGGCTGGCAGAAATGCTATGCACTTCTATGGTGGTGGATGCTCTGGC 126			
QY 61	ACCATGGGTGGACCTGTGGGTATGGAAATTTATACACCAAGGATATGCGACGACACG 120			
Db 127	ACATATGGGGGGTCTCTGTGATATGGAATTTATATACCAAGGATATGACACCACTACT 186			
QY 121	GTCGCGCTGAGCACTGCGCTATTTAACATGGATTAAGTTGTGTGTGCTGCTTGGAAATG 180			
Db 187	GCAGCACTAAGTACAGCACTATTCAACATGGTTTAACATGGGGCTTTGTACGAGCTG 246			
QY 181	ACTGTACAAAGAGCCCTAAATGTCCTTCCGGAACTATAGGTCACTGCGACCAAC 240			
Db 247	ACTTGCACAAAGATGTGTCATCGCTCCGACGAGGAGCATTTATGTACTGCACATCAAC 306			
QY 241	TTTTGGCCTCCTACCTTGTCTCCCTCAACAACAATGATGATGTCGACCAACCTCCTC 300			
Db 307	TTCTGGCCTCAAAATCAATCCCTCCCTAACACATGATGTTGTGTCATCCCTCTC 366			
QY 301	CAACACTTGCATATGGCTGAGCTGCTCTCTCTTCAATGCTCAATACGAGCTGTATC 360			
Db 367	CACACTTGTGATTTAGCTCACGCTGCTTTCTTGCAAAATGCCAAATACAGACTGGAAATC 426			
QY 361	GTCGCCGTCCTCTTTCGTAGGGTACCATGTATGAAAGAAAGTGGAGTGGTTCAATC 420			
Db 427	GTCTCTGTTCTTCCGAAAGGTCCTCTGACGAGAAAGGGGAGTAAGTTTACATTA 486			
QY 421	AATGGCCACTATACCTTCAACCTCGTTTGTATCACAAGCGTGGTGGCCAGCGACGCTC 480			
Db 487	AATGGACACTATCTTCAACTGGTTTGTGACAAATGTTGGGGGTCCGGGTATGTT 546			
QY 481	CACCTCTGTGTGATTAAGGGGTCTCGAAGCGATGGATGCATGTCTTAGAAATTTGGGGC 540			
Db 547	CAATCAGTTTCAATTAAGGTTCAATTAAGTGTGATGATGAGGAGTATGCAAAATTTGGGGC 606			
QY 541	CAAAACGTGGCAAGCAACAACATATCTCAATGGCCAGGCGCTTCTCTTCAAGTCACTCTT 600			
Db 607	CAAAACGTGGCAAGCAACAACATCTCAATCTCAATGGCCAGAGCTCTTCAATTCAGTCAACCACT 666			
QY 601	AGTATGATGTGCACACTGCTCACTGCTATATCTGTTCCCTGCAATTTGGCAATTTGGCCAA 660			
Db 667	AGTATGATGATGATCTCTCACTAGCAACAATGCTGACAGCAAAATTTGGCAATTTGGCCAA 726			
QY 661	ACCTATGAAGGCCCTCAATT 680			
Db 727	ACTTTTGAAAGGGGCTCAATT 746			
RESULT 9	AF297521			
LOCUS	AF297521	1048 bp	mRNA	linear
DEFINITION	Prunus avium expansin 1 (Exptl) mRNA, complete cds.			PLN 17-SHP-2000
ACCESSION	AF297521			
VERSION	AF297521.1	GI:10180016		
KEYWORDS				
SOURCE	sweet cherry.			
ORGANISM	Prunus avium			



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1048)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 1048)  
Mu, Z. and Wiersma, P.A.  
Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening  
Unpublished

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Mu, Z. and Wiersma, P.A.  
Direct Submission  
Submitted (18-AUG-2000) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, 4200 Highway 97, Summerland, British Columbia V0H 1Z0, Canada

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Location/Qualifiers

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BASE COUNT 281 a 245 c 234 g 288 t  
ORIGIN  
Query Match 62.7%; Score 427.2; DB 8; Length 1048;  
Best Local Similarity 76.8%; Pred. No. 1,8e-120;  
Matches 522; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 1 GACTACGCTGGCTGGCAGAGCGGCGACCTTTATGCTGGTGCAGCATCGGC 60  
DB 162 GATATATGCTGGCTGGAGAGCGCTCATGCTTTATGCTGGCTGCATCGCGGA 221  
QY 61 ACCATGGCTGGAGCTTGGCTATGGAATTTATACGCCAAGGATATGGCAGAAC 120  
DB 222 ACAATGGGGGAGCATGTGGTATGGACCTTGACAGCCAGGATATGGAACCAACT 281  
QY 121 GTGCGCTGAGCACTGGCTATTAAACAATGATTAAGTGTGCTGCTTCAATG 180  
DB 282 GCACCTTTAAGCAGACGCTTGTATTAACAATGGCTGAGCTGCTTGTATGAATG 341  
QY 181 ACTTGTACAAGACCTTAATGCTGCTTCGCGAAGCTATAGGCTCACTGCCACAC 240  
DB 342 AGATGCAACAATGACCTTAGATGTGTCGTCGGAAGCATCTTGTACTGTACAAAC 401  
QY 241 TTTTGGCTCTCAATTTGCTCTCCCTAACAAATGATGATGATGCAACCTCTCTC 300  
DB 402 TTTTGGCCCACTTAATTTGCTCACTCCAAAGATTAAGGCGCTGATCAATCTCTCTC 461  
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DB 462 CAGCACTTTCATTTGGCCGAGCTGCTTCTTCAATATGCCCAATACGCGCTGGATT 521  
QY 361 GTCCCGCTCTCTTTCGATGAGTATGAAAGAGGATGATGATGATGATGATGAT 420  
DB 522 GTCCCTGTTACCTTCAAGAGAGTGCCTGATGAAAGAGGATTAAGATTCACATC 581  
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DB 582 AATGGCACTACCTTCACTCACTGATGATGATGATGATGATGATGATGATGATGAT 641  
QY 481 CACTGTGTGATGAAGAGGCTTCGAGCTGATGATGATGATGATGATGATGATGATGAT 540  
DB 540 CACTGTGTGATGAAGAGGCTTCGAGCTGATGATGATGATGATGATGATGATGATGATGAT

DB 642 CATTCACTTCAATCAAGGATCCAGAACAGGCTGGCAACCCATGTCAGAAACTGGGG 701  
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DB 702 CAAAACGTGGCAAGCAACAATATTCATGATGCGCAAGGCTTCTTCAATGACTCTTT 761  
QY 601 AGTATGCTGGCACTGCTCACTGCTTATATCTGTTCTTCAATGCGCAATTTGGCCAA 660  
DB 762 AGTACGAGGAAGACTGTCACAACTGACAGTGGCCCTGATGATGATGATGATGAT 821  
QY 661 ACCTATGAGGCCCTCAATT 680  
DB 822 ACTTCTCAGGGGCTCAATT 841

RESULT 10  
AF350937 1109 bp mRNA linear PLN 01-MAY-2001  
LOCUS  
DEFINITION  
Prunus cerasus expansin (EXP2) mRNA, complete cds.  
AF350937  
VERSION  
AF350937.1 GI:13898650  
KEYWORDS  
SOURCE  
Prunus cerasus.  
ORGANISM  
Prunus cerasus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1109)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 1109)  
Yoo, S.-D., and van Nocker, S.  
Direct Submission  
Submitted (19-FEB-2001) Department of Horticulture, Michigan State University, 392A Plant and Soil Science Building, East Lansing, MI 48824, USA

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BASE COUNT 308 a 251 c 239 g 311 t  
ORIGIN  
Query Match 62.7%; Score 427.2; DB 8; Length 1109;  
Best Local Similarity 76.8%; Pred. No. 1,8e-120;  
Matches 522; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 1 GACTACGCTGGCTGGCAGAGCGGCGACCTTTATGCTGGTGCAGCATCGGC 60  
DB 156 GATATATGCTGGCTGGAGAGCGCTCATGCTTTATGCTGGCTGCATCGCGGA 215  
QY 61 ACCATGGCTGGAGCTTGGCTATGGAATTTATACGCCAAGGATATGGCAGAACAG 120  
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Db	276	GCACCTTTAATCACAGCCTTGTATTAACATATGGCTTGAGCTGTGGCTCTTGTATTGAATG	335
OY	181	ACTGTGCAAAACGACCCTTAATATGGTGCCTTCCGGGAACTATTAGAAGTCACTGCCAACAC	240
Db	336	AGATGCAACATATGACCATAGTAGTGGTGTGCTCTGGAAACATCATGTATTGCTACAAAC	395
OY	241	TTTTGCCCTCTTAACCTTTGCTCTCCCTAACAAACAATGSGATGSGTGAACCTCTCTC	300
Db	396	TTTTGCCCACTTAACCTTTGCTCAAGTCCAAACGATATGCGCTGGTGCATATCTCTCTC	455
OY	301	CACACTCCGACATGGCGTGAAGCCTGGCCCTTCCTCAATCGCTCAATFACGAGCTGGATC	360
Db	456	CAGACCTTTGATTTTGGCCGAGCCTGCTCTTCTTGCAAATATGCCCAATACCGCGCTGGATT	515
OY	361	GTCGCCGCTCTCTCTTCTGAGGGTACCATGATATGAAGAAGGTGAGTGAAGGTTTACAATC	420
Db	516	GTGCGCTGTACTCTTACAGAAAGTGGCCCTGTATGAAGAAGGAGNAATAAGATTCCACATC	575
OY	421	AATGGCCAATCAATCTTAACCTCGTTTGTATCACAAACGTCCGGTGGCGAGCGACCTC	480
Db	576	AATGGCCAATCTCTTAACCTCGTTTGTATCACAAACGTGGGTTGGTGCAGGAACCTC	635
OY	481	CACCTGTGTGATTAAGGGGTCTGAAGCTGGATGGCATCATCTATCTAAGAAATTTGGGGC	540
Db	636	CATTGATGTTTCATATAAAGGATCCGAAMCAGSGTGGSCAACCATCTCAAGAAACGTGGGG	695
OY	541	CAAACTGGCAAGCACAACACTATCTCAATGGCCAGGCGCTTCTCTTCAAGTCACTCTT	600
Db	696	CAAACTGGCAAGCACAACACTATCTCAATGGCCAGGCGCTTCTCTTCAAGTCACTCTT	755
OY	601	AGTATGTTGTCGACTCTACATGCCATATATCTGCTTCCATTTGGCAATTTGGCCAA	660
Db	756	AGTGCAGGAAGACGTGCACAAACTRACACAGTGGCCCCGTGTAATTGGCATTTTGCTAG	815
OY	661	ACCTATGAAGGCGCTCAATT	680
Db	816	ACTTCTCAGGGGGTCAATT	835
RESULT 11			
LOCUS	AF350936	1233 bp	mRNA linear
DEFINITION	Prunus cerasus expansin (EXPI) mRNA, complete cds.		PLN 01-MAY-2001
ACCESSION	AF350936		
VERSION	AF350936.1	GI:13898648	
KEYWORDS			
SOURCE	Prunus cerasus.		
ORGANISM	Prunus cerasus.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
TITLE	Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.		
JOURNAL	Yoo,S.-D., Gao,Z., Cantini,C., Loescher,W. and van Nocker,S.		
REFERENCE	Coordinated expression of genes encoding expansins and other cell		
AUTHORS	wall-modifying enzymes is associated with pectin-related changes in		
TITLE	the cell wall during ripening of cherry ( <i>P. cerasus</i> ) fruit		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1233)		
AUTHORS	Yoo,S.-D. and van Nocker,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-FEB-2001) Department of Horticulture, Michigan State		
	University, 392A Plant and Soil Science Building, East Lansing, MI		
	48824, USA		

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BASE COUNT	327 a	253 c	302 g	351 t			
ORIGIN							
Query Match	61.8%;	Score 420.6;	DB 8;	Length 1233;			
Best Local Similarity	76.4%;	Pred. No. 1.9e-118;					
Matches 516;	Conservative 0;	Mismatches 159;	Indels 0;	Gaps 0;			
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DB	261	CTCAGCACAGCTCTGCTTCACAGATGGCTGTGAGCTGTGGGTATGTATGAGATGAGATGT	320				
QY	187	ACAAGCACCCCTAAATAGTGTGCTTCCGGGAGCACTTATAGGTGATGCGCACCAACTTTTGC	246				
DB	321	GACAGTACCCCAATAGTGTGCTTCCCGGACAGCATCATGTCACCCCAAACTTCTGC	380				
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LOCUS							
DEFINITION							
ACCESSION							
VERSION							

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

*Fragaria x ananassa*.  
*Fragaria x ananassa*.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustroids I; Rosales; Rosaceae; Rosoidae; Fragaria.  
1 (bases 1 to 1180)  
Civello, P.M., Sabehat, A., Powell, A.L.T. and Bennett, A.B.  
An expansin gene expressed in ripening strawberry fruit is  
auxin-independent  
Plant Physiol. 12 (4), 1273-1279 (1999)  
2 (bases 1 to 1180)  
Civello, P.M., Sabehat, A., Powell, A.L.T. and Bennett, A.B.  
Direct Submission  
Submitted (16-JUN-1999) Dept. of Vegetable Crops, Univ. of Calif.  
Davis, Mann Lab, Davis, CA 95616, USA  
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BASE COUNT 292 a 262 c 290 g 336 t  
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Query Match 61.3% Score 417.6; DB 8; Length 1180;  
Best Local Similarity 75.9%; Pred. No. 1.6e-117;  
Matches 516; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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QY 62 CCATGGGTGAGCTTGTGGTATGGAATTTATACAGCCAGGCTATGCGACAGACGG 121  
DB 184 CAATGGAGGTGATGTGATGAACCTTGTACAGCCAGGCTATGAGACCAACACTG 243  
QY 122 TGGCGGTGAGCACTGGCTATTATTAACATGATTAAGTTGTGCTCTTGAATAA 181  
DB 244 CAGCACTTACAGACAGCTCTGTTACAGATGCTTGAGCTGCGGCTTCTTCTACGAATGC 303  
QY 182 CTGTGACAAACGACCTTAATGCTGCTTCGGGAACTATTAGGCTCACTGCCACCACT 241  
DB 304 GATGTACACATGACCTAGATGCTGCTTCGGGAACTATCATGTCACCGCCACCAACT 363  
QY 242 TTTGGCCTCTACTTGTCTCCCTAACACAAAGTGGATGAGTGCACCTCTCTCC 301  
DB 364 TCTGCCCTCCCACTTGTCTCAGAGCCAAATGACAGCGTGGTGCACACCTCTCCCTCC 423  
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RESULT 13  
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LOCUS AF096776  
DEFINITION Lycopersicon esculentum expansin (leexp2) mRNA, complete cds.  
ACCESSION AF096776  
VERSION AF096776.1 GI:3747131  
KEYWORDS  
SOURCE  
ORGANISM  
tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; easterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 1147)  
Catala, C., Rose, J.K.C. and Bennett, A.B.  
Auxin-regulated genes encoding cell wall-modifying proteins are  
expressed during early tomato fruit growth  
Plant Physiol. 122 (2), 527-534 (2000)  
JOURNAL MEDLINE 20144019  
PUBMED 10677445  
REFERENCE 2 (bases 1 to 1147)  
Catala, C., Rose, J.K.C. and Bennett, A.B.  
Direct Submission  
Submitted (02-OCT-1998) Vegetable Crops, University of California  
Davis, CA 95616, USA  
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BASE COUNT 312 a 208 c 235 g 392 t  
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Matches 514; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

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Oy	121	GTGGCGCTGAGCACCTGGCGTATTTAACATGATTAAGTTGGTGGCTTGC	180
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Oy	181	ACTTGTACAAACGACCCATAAATGTCCTTCGGGACATATTAGGTCAC	240
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Oy	241	TTTTCGCTCCATACTTGTCTCCCTTAACAAACATGGTGGATGGTGGCA	300
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Oy	301	CAACACTTCGACATGGCTGAGCCTCCCTTCAATTCGCTCAATPACGAGCTG	360
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Db	538	AATGACACCTCAATTTTTCAACTTGGTTTAGTGAACAATGTTGGAGG	597
Oy	481	CACCTGTGTGCATTAAGGGGCTCGAACCTGGATGGCAATCCATCTCT	540
Db	598	CAATCAGTTTCAATTAAGGGGTCTAATCTGGATGGCAAGCAATGTCA	657
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Db	718	ACTGTAGTGAAGACACTCTATAGCAACAATCTGCACCAAAATTAAT	777
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AF230332 RESULT 14
LOCUS AF230332 1088 bp mRNA linear PLN 26-JUN-2000
DEFINITION Zinnia elegans expansin 2 mRNA, complete cds.
ACCESSION AF230332
VERSION AF230332.1 GI:7025492
KEYWORDS
SOURCE
ORGANISM
Zinnia elegans.
Zinnia elegans.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Asteridae: euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.
1 (bases 1 to 1088)
Im.K.H., Cosgrove,D.J. and Jones,A.M.
Subcellular localization of expansin mRNA in xylem cells
Plant Physiol. 123 (2), 463-470 (2000)
20317189
MEDLINE
PUBMED
10859177
REFERENCE
2 (bases 1 to 1088)
Im.K.-H., Cosgrove,D.J. and Jones,A.M.
Direct Submission
Submitted (02-FEB-2000) Biology, University of North Carolina,
Chapel Hill, NC 27599, USA
JOURNAL
Location/Qualifiers
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FEATURES
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STIC-Biotech/ChemLib

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From: Saidha, Tekchand  
Sent: Wednesday, October 09, 2002 5:40 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request - 09/896301

09/896301

Please search the data base & interference files :

SEQ ID NO : 1 through 7

Thank you !

*Tekchand Saidha*  
*Primary Examiner*  
*Art Unit 1652, CM1, Room No. 10D05*  
*Mail Box 40601*  
*(703) 305-6595*

10D01

Point of Contact  
P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 10/16/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
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AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
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Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
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Other (specify): \_\_\_\_\_

